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AX392417

1321 bp from Patent WO0216416.

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PAT 23-MAR-2002

AX392417.1

SOURCE ORGANISM

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa;

KEYWORDS

REFERENCE

ɗammalia;

TITLE

Diagnosis

and treatment of cardiovascular conditions

Landschulz, K.T., Kennedy, S.P.,

Thompson, J.F.

; Metazoa; Chordata; Craniata; Vertebrata; l Eutheria; Primates; Catarrhini; Hominidae;

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Homo.

Lee, R.T., Turi, T.G. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. a 000 0000 000 a a a Query Match 100.0 93.0 65.2 63.4 60.6 333333 .6 110000 .6 112883 .6 118959 .6 153308 61505 130435 15833 150224 408 693 812 51 651 878 1376458 175754 175363 219471 221100 233939 237026 237151 198689 258632 249554 176821 Length 1818 BB AX199565 0 AF220208 AX392428 0 BC036995 0 AL837509 0 AC110189 0 AC134911 AC1139417 AC111878 AX392431 AC110189 AC116815 OSJN00235 AC118668 AC126463 AX655988 HSAJ757 AX392430 AX011709 HSJ1059L7 AX071267 HS718J7 Ħ AY128643 SUMMARIES ALIGNMENTS AX525744 Sequence AC139417 Rattus no AC111878 Rattus no AX392431 Sequence AC116815 Mus muscu AC655988 Sequence AJ000757 Homo sapi AB065453 Homo sapi AC106698 Rattus no AC0106498 Rattus no AC0126463 Rattus no AC118668 Genomic s AC126463 Rattus no AC112841 Rattus no AC112848 Rattus no AC112848 Rattus no AC137424 Rattus no AC137427 Rattus no AC137428 Rattus no AC137327 Rattus no AC137328 Rattus no AC105358 Rattus no BC015918 Homo sapi AF224278 Homo sapi AY128643 Homo sapi AF305426 Homo sapi AL035541 Human DNA AX392428 Sequence BC036995 Mus muscu AL837509 Mouse DNA AX011709 Sequence AX199565 Sequence AF220208 Mus muscu Description AC134911 Mus muscu AL837520 Mus muscu AC110189 Mus muscu AX071267 Sequence AX392430 Sequence AX392419 Sequence Human DNA Homo sapi

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                                               AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4839)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Characterization of a novel gene, STAGI/PMEPA1, upregulated
renal cell carcinoma and other solid tumors
Mol. Carcinog. 32 (1), 44-53 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGT
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                                             submitted (14-SEP-2000)
                                                      Rae, F.K., Hooper, Direct Submission
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Diagnosis and treatment of cardiovascular conditions patent: wo 0216416-A 3 28-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER LOCALION/Qualifiers
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Eutheria; Primates;
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RESULT 4
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            Homo sapiens, clone MGC:20374 I
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AUTHORS
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hislao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. COD DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bogsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian Submitted (15-OCT-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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Mammalia; Eutheria;
1 (bases 1 to 1061)
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Strausberg, R.
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/lab_host="DH10B-R"
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Direct Sub
Submitted
                                                                                            Moul,J.W. and Srivastava,S.
A novel androgen-regulated gene, PMEF
20q13 exhibits high level expression
Genomics 66 (3), 257-263 (2000)
                                                                                                                                                                                                                                                Homo sapiens PMEPA1 protein
AF224278
AF224278.1 GI:9255808
           Xu,L.L., Shanmugam,N., Se
Moul,J.W. and Srivastava,
Direct Submission
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1141)
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            CGTGCTACGGCAGCGGCGCGCATGGAGGGGCCGCCCCCCCTACAGCGAGGTCATCG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.31-13.33"
/cell_line="LNCaP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="PMEPA1 protein"
/protein_id="AAF66322.1"
/protein_id="AAF66322.1"
/db_xref="Gi:925809"
/translation="MAELEFVQIIIIVVVMVWVVITCLLSHYKLSARSFISRHSQG
/RREEDALSSEGCLMPSESTYSGNGIPEPQVYAPPRPTDRLAVPPAQRERFHRPQPTY
PYLQHEIDLPPTISLSDGEEPPPYQGPCTLQLEDPEQQLELNRESVRAPPNRTIFDSD
LMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPP
SLLEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PMEPA1"
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Submitted (03-JUL-2002) Department of Medicine, Case Western ...
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/translation="MAVMYVITCLShyklsarsfire"
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/db_xref="taxon:9606"
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                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 61505)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Identification and characterization of a novel gene up-regulated in renal cell carcinoma and other soli
                                                                                                                                                                                                                                     Homo sapiens solid tumor-associated complete cds. AF305426
                Unpublished
                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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Euteleostomi; Homo.

gene, solid

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IIIVVVMMYMYVVITCLLSHYKLSARSFISRHSQGRRREDALSSEGCLWPSESTVSGN
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join(1. 429,50206. .50360,56817. .56870,57305.

jgene="STAG1/PMEPA1"

/product="solid tumor-associated 1 protein"

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/gene="STAG1/PMEPA1"
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/db_xref="taxon:9606"
/chromosome="20"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; TI:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the entire insert of clone RP4-718J7 The true end of clone RP5-1007E6 is at 71437 in this sequence. The true right end of clone RP4-579F20 is at 43945 in this sequence. RP4-718J7 is from the library RPGI-4 constructed by the group o Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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On Dec 5, 2000 this sequence version replaced gi:10198628.
During sequence assembly data is compared from overlapping clones
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/chromosome="20"
                                                                                                                                                                                                                                                                                                      /mol_type="genomic
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/mol_type="genomic DNA"
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/note="4
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/note-"Charliel repeat: matches 681. .781 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /wote="5 copies 54 mer 75% conserved" 2583. .2716 'Copies 67' 'Cop
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                                                                                                                13585. .13716
/note="22 copies 6
13586. .13717
                                                                                                                                                                                                                                                    note="LIMD2 repeat: matches 6032. .6331"
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                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJb repeat:
10658. .10753
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                                                         'note="66 copies 2 mer tc 68% conserved"
13588. .13715
                                                                                                                                                                                                'note="3 copies 56
                                                                                                                                                                                                                                                                                 'note-"LTR19B repeat: matches 1. 2519. .12813
                                                                                                                                                                                                                                                                                                                                                                 'note="L2 repeat: matches 2647. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"AluJb repeat: matches 188. .300 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0880. .10089
note="12 repeat: matches 2292. .2511 of consensus"
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note="L1MB4 repeat:
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2028. .2632
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                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1.
                            78% conserved"
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AGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCCGTTCGCCC
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="macun: 21663; complement(21278. .21663; /note="match: GSS: Em:AQ136459" /note="match: GSS: .21672; .21672; /note="match: 21392. .21672; /notes="match: 21672; /notes="match: 21683; /notes=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="34 copies 4 mer cttt 77% conserved"
complement(13622. .14142)
/note="match: GSS: Em:AQ592603"
14313. .14437
/note="LTR15C repeat: matches 257. .386 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21667. .21775
/note="MIR repeat: matches 73. .192 of
                                                                                                                                                                                                                                                            /note="L1MB5 repeat:
32224. .32522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(21392.
/note="match: GSS
21667. .21775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ748384" complement(21187. .21672)
                                                                                                                                                                                                                        /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                   'note="FLAM_C repeat: matches 1. .127 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 38. .242 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2336. .2710 of 25580. .25611 copies 2 mer tc 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 90. .143 complement(21005. .21672)
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20413. .20463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MIR repeat: matches 138.
18585. .18776
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L8312. .18438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="2 copies 32 mer 98% conserved"
16575. .16690
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/note="14 copies 6 mer cacaca 82% conserved"
15029. .15108
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15026. .15109
/note="7 copies 12 mer 82% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5021. .15110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER20 repeat: matches 7.
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3. .15399
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100.0%;
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Pred. No.
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278. .21663)
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                                                                                                                                                                                                                                                                                       matches 6015. .6176 of consensus"
                                                                                                                           DB 9;
1e-294;
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                                                                                                                                                        Length 130435;
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Mammalia; Eutheria;
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                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
469 c 457 g 29
                                                                                                                                                                                                                                                                        Location/Qualifiers
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Primates;
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Pred. No. 1.1e-277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone RP5-1059L7 on chromosome 20q13.2-13.33 Contains the 5' end of the TMEPAI (PMEPAI) gene encoding an androgen induced 1b transmembrane protein, ESTs, segss and two CpG islands, complete segmence
                                                                                                                                                                                                 only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-1059L7 The true left end of clone RP11-402F1 is at 106677 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
on Mar 6, 2000 this sequence version replaced gi:7007305.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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/note="L2 repeat: matches 2616. .2707 of consensus"
complement(2445. .53425)
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/gene="TMEPAI"
                                                                                                                                                                            /db_xref="Sptrembl:Q9ntr9"
/translation="MGVNSTAAAAAGQPNVSCTCNCKRSLFQSMEITELEFVQIIIIV
/VMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSS"
                                                                                                                                                                                                                                                 /evidence-not_experimental /product="dJ105917.1.1 (androgen induced type transmembrane protein (PMEPA1), isoform 1)" /protein_id="CAB88144.1"
                                                                                                                                                                                                                                                                                                                                            /note="continues in dJ718J7 (AL035541) match: proteins: Tr:015166 Tr:015168"
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complement(join(<2445. .2599,52376. .52472))
/gene-"TMEPAI"
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/product="dJ105917.1.2 (androgen induced type
transmembrane protein (PMEPA1), isoform 2)"
/protein_id="CAG32857.1"
/db_xref="GI:13160408"
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(mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3573. .3697
"note="5 copies 38 mer 64% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="19 copies
3394. .3893
/note="25 copies
                             /note="MIR repeat: matches 117.
23231. .23438
                                                                                                                                                                                                                  19070. .19291
/note="MIR repeat:
19954. .20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14448. .14493
/note="23 copies 2 mer at 76%
14634. .14813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5002. .5190
/note="MER20 repeat; matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3473. .3904
/note="12 c
                                                                   /note="L2 repeat: matches 2322.
23102. .23203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3103. .8205
/note="MIR repeat: matches 48. .161 of consensus"
complement(8858. .9277)
                                                                                                                                                            /note="L2 repeat: matches 2581.
                                                                                                                                                                                                                                                                                                             /note="match: GSS:
                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 2679.
17699. .18179
                                                                                                                                                                                                                                                                                                                                                                                   /note="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    15690. .15935
/note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 11. .196 of consensus" 11630. .12037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Charlie4 repeat: matches
11175. .11343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224. .5282
note="MIR_repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 792. .5001
/note="3 copies 70 mer 82% conserved"
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                                                                                                                                                                                                 'note="L2 repeat: matches 2358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: GSS: Em:AQ881699"
)224. .9382
                                                                                                                      note="L1MD2 repeat: matches 5595. .6341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"AluSx repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="MER20 repeat: matches 1.
                                                                                                                                                                                                                                                                         ="MIR repeat: matches 107. .243 of consensus"
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           repeat: matches 3.
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                                                                                                                                                                                                                                    matches 35. .261 of consensus"
                                                                                                                                                                                                                                                                                                          Em: AQ703107"
                                                                                                                                                                                                                                                                                                                                                                                                                          matches
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RESULT 11
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Sequence 1739 from Patent W00102568.
AX071267
AX071267.1 GI:12581618
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Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crai
Human genes and gene expression products
                                                     Williams, L.T.,
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                            Homo
                                                                                                                                                                                                                                                                         GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCA 521
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                                                                                                         sapiens (human)
sapiens
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24752. .25042
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24460. .24580
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29374. .29501
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26450. .26485
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                                                      Escobedo, J.,
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Pred. No. 1.7e-257;
0; Mismatches 0;
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                                                     Innis, M.A., Garcia, P.D.,
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              Strache-Crain,
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                                                                                              Euteleostomi;
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                                                  Klinger,J.,
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Sequence 14
AX392430
AX392430.1
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                                                                                                                                                         Diagnosis and treatment of cardiovascular conditions Patent: WO 0216416-A 14 28-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER
                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; M
                                                                                                                                                                                                Turi,T.G.
                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                      Similarity
                                                                                                                                                                                                           Lee,R.T., Landschulz,K.T., Kennedy,S.P.,
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
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159 c 115 g 5
                                                                                    /organism="Homo sapiens"
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205 c 237 g 14
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SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilarsky,C
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
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AX199565
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                                               Direct Submission
Submitted (30-DEC-1999) Division
Cancer Research, IMVS, Frome Rd,
Location/Qualifiers
                                                                                                                                                Biochem.
20498735
                                                                                                                                                                                                                                                                                                                      Mus musculus Nedd4 WW domain-binding AF220208
                                                                                                                                                                                      Jolliffe,C.N., Harvey,K.F., Haines,B.P., Parasivam,G. and Kumar,S. Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligas.
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 651)
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Mammalia; Eutheria; Primates;
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Jolliffe,C.N. a
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                               of Haematology, Hanson Centre
Adelaide, SA 5000, Australia
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Match
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                                                                                                                                                                                                                                                                                                           is the number of results predicted by chance to have a iter than or equal to the score of the result being printed, ived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA201A.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA201B.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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ABK12137
ABK92120
AAI57868
AAA75151
AAA47429
ABZ36103
AAA75163
AAA75164
                                                                                                                                                                                                                                                                    SUMMARIES
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8572.014 Million cell updates/sec
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cDNA encoding a hu
Sequence encoding
Human secretory po
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  cDNA clone
                                                                                                                                                        Human cDNA encodin
                                                                                                                                   Prostate cancer-as
  encodin
encodin
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ALIGNMENTS

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RESULT 1
ABK12137
 CDS
                                                                                                                                                                                       Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arterioscleros
                                                                                                                                                          Homo
                                                                                                                                                                                                                                              Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
                                                                                                                                                                                                                                                                      05-JUN-2002
                                                                                                                                                                                                                                                                                                                 ABK12137 standard; cDNA; 1321
22-AUG-2000; 2000US-227159P
                     21-AUG-2001; 2001WO-US26089
                                                               WO200216416-A2.
                                                                                                                                                                                                                                                                                            ABK12137;
                                           28-FEB-2002.
                                                                                                                                                                                heart failure.
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                                                                                     /product-
/note- *Th
                                                                                                                    Location/Qualifiers
413..1276
                                                                                                            /*tag=
                                                                                   "t= "MIVR-1"
"This region is specifically claimed in claim
                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                        stroke; arteriosclerosis;
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The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MYVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC they are not identical to Genbank sequences AI761441.1, AI594390, CC NM,004338 and AQ177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDUP-1 BTG-2 and TIS-11d or its CC expression product, determining if the anti-apoptotic activity is CC expression product, determining if the anti-apoptotic activity is CC expression of such disease and nucleic acids of the invention are useful for CC apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and CC disorders as characterised by increased apoptotic cell-death of vascular cendothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC stroke, arteriosclerosis and heart failure. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 1321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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DB; AAU78231.
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   481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
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                                                                                                                     GGCGCAGCGCGCCCCCCCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCACTGCCG
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CTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGCCGGGCAGCCCAATGTCTCCTGCAC
                                                                                                                                                  ACGCCCCCGGGGCTGCCGAGGGGAGGCCGGGGGGGGGGCGCAGCGGAGCGCGGTCCCGCGCAC
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RESULT 2
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DE Pros
XX
KW Pros
KW gene
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OS Mamm
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                                                                                         Prostate cancer-associated
                                                                                                                                                    ABK92120
                                                         Prostate cancer; prostate tumour tissue;
                                                                                                                      15-AUG-2002
                                                                                                                                                                                  ABK92120
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                                           therapy; gene;
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                                                                                                                      entry)
                                                                                         DNA sequence
                                                            human;
                                                            mammal;
                                                           cytostatic;
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Matches 800;
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24-JAN-2001;
16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
                                                                                                                                                                                                                                                                                                                       The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gish
                                                                                                                                                                                                                                                                                identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polynucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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are expressed
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           762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Page 305; 436pp; English.
                                                                                                                                                                                                                 Similarity
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                                                                                                                             TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
                                                                                                                                                           1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g a prostate cancer-associated transcript in a cell in a useful for diagnosing prostate cancer (PC) or screening rs of PC, by determining if prostate cancer-associated gessed in a prostate tissue -
                              GCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGTCTACGCCCCGGCCTCGGCCCACCG
                                                                                   GCCAGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
          ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT
                                                                         GCCAGGGGCGGAGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA
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2001US-263957P.

2001US-276791P.

2001US-27688P.

2001US-281922P.

2001US-286214P.

2001US-0847046.

2001US-0847046.
                                                                                                                                                                                                     60.6%;
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09-JUL-2000;
19-JUL-2000;
19-AUG-2000;
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19-OCT-2000;
                                                                                                                                                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis: inflammaticalenikaemia.
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Zhao
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He sequence data for this patent did not form part of the printed.
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Xu C, Xue AJ,
R, Drmanac RT;
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                                                             Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                       Barnes TM,
                                                                                                                                                                                                                                                                                                              01-MAR-2000; 2000WO-US05226
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Claim

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Fig

5; 175pp; English

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cc proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand cc factor-associated disorder, regulate extracellular matrix structuring, cc cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative cc disorders, such as cancer, modulate the proliferation, differentiation, cc and/or function of cells that appear in the bone marrow, and leukocytes, cc treat bone marrow, blood and hematopoletic associated diseases and confict bronchitis, bronchial asthma and bronchiectasis, intestinal cc disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral codema, hydrocephalus, brain herniations, latrogenic disease, cerebral toxoplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 799
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Pred. No. 0;
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11-DEC-1998;
09-FEB-1999;
16-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron associated protein; NEUAP; neurological disorder; epilepsy; ischemic cerebrovascular disease; stroke; cerebral neoplasm; Alzheimer's disease; Pick's disease; Huntington's disease; dementia; Parkinson's disease; demyelinating disease; meningitis; prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
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                       Claim 9;
                                                         New human neuron-associated proteins and useful for diagnosis, treatment and prevent
                                                                                                                                                                                                                                                                                  15-JUN-2000.
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                     Page 136; 145pp; English.
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                                              neurological disorders
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Pred. No. 0;
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19-JUN-2001;
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20-JUN-2001;
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29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; histelmer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-filammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; antiporvalic; antiporvali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                             New human secretory proteins and poldiagnosing, treating or preventing a (e.g. AIDS), neurological disorders
                                                                                                                                                                                                                                                                                                                                Daughtery SC, Dam TC, peralta CH, David MH, Flores V, Marwaha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2002;
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JE, Hillman JL, Yu JY, Tua

TY SC, Dam TC, Liu TF, Ng

TY SC, Dam TC, Liu TF, Ng

TY SC, Tan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCYTE GENOMICS INC.
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2001US-291829P.
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TF, Nguyen I
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                                                                                                polynucleotides, useful for ng autoimmune/inflammatory discers (e.g. Alzheimer's), or cell
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n O, Yap PE, Ar
n DA, Kleefeld 1
n AJ, Panzer SR.
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AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

Disclosure; Page -; 175pp; English.

AAA75163-65 encode human TANGO 261 proteins. The specification also CC describes TANGO 266, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The CC cellular differentiation and/or modulate cellular adhesion. The CC disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, cc modulate cell adhesion in proliferative disorders, such as cancer, CC modulate the proliferation, differentiation, and/or function of cells cc modulate the proliferation, differentiation, and/or function of cells cc ashma and bornochiectasis, intestinal disorders, atelectasis, pronchital cc unimonary congestion or cedema, emphysema, chronic bronchitis, bronchial cc diseases, modulate renal disorders, treat cardiovascular disorders such cc as ischemic heart disease, modulate the proliferation, differentiation, can allow for function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bacterial and viral meningitis, Alzheimer's blsease, cerebral coccephalus, brain herniations, laterogenic disease, inflammations, bacterial mand annother annother than treat herafic disorders.

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Pred. No. 1.5e-303;
0; Mismatches 2;
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Query Match Best Local S Matches 798

Similarity

52.8%; 99.8%; ð, 317

Score 698; DB 21; Pred. No. 1.5e-303;

Length Indels

969;

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Gaps

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0;

Mismatches

Sequence

969 BP;

210

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294

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148 T; 0 other;

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disorder, regulate extracellular matrix structuring, cellular adhesion, cc and cell trafficking and/or migration, modulate cellular interactions, cc modulate cell adhesion in proliferation, adifferentiation, and/or function of cells commodulate the proliferation, differentiation, and/or function of cells ct that appear in the bone marrow, and leukocytes, treat bone marrow, blood cc and hematopoietic associated diseases and disorders, atelectasis, cc pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial cc asthma and bronchiectasis, intestinal disorders, spleen associated cd diseases, modulate renal disorders, treat cardiovascular disorders such cas ischemic heart disease, modulate the proliferation, differentiation, cc and/or function of bone and cartilage cells and to treat bone and/or cc cartilage associated with the ovaries, and cerebral oedema, chydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral corcephalus and encephalitis, and treat hepatic disease, brain cancers, cc hydrocephalus and encephalitis, and treat hepatic disease, cerebral concers, parkinson's disease, multiple sclerosis, brain cancers, conceit the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any you Willebrand factor associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261 262, 266 and 267 useful as modulating agents of cellular processes. e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1999;
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/product=
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                Human; ss; prostate specific nucleic acid; PSNA; cytostatic; non-cancerous prostate disease; PSP; prostate specific protein; metastasis.
                                           Prostate
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                                                                               ABS61424 standard; cDNA; 1583
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                                           nucleic acid DEX0259_32.
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                           prostate vaccine;
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The invention relates to an isolated polypeptide comprising a sequence CC with 60 % identity to one of prostate specific protein (PSP) sequences, CC or comprising an amino acid sequence encoded by one of 136 nucleotide CC or comprising an amino acid sequence encoded by one of 136 nucleotide comprising the wector comprising the polynucleotide, a host cell CC comprising the vector comprising the polynucleotide. The specification CC comprising the protein or polynucleotide. The PSP and PSNA are CC vaccine comprising and monitoring the presence and metastases of CC useful for diagnosing and monitoring the presence and metastases of CC prostate cancer in a patient. The PSNA is useful for determining the presence of prostate specific protein in a sample, and CC determining the presence of prostate specific protein in a sample, and CC determining the prostate cancer, which induces an immune CC polypeptide and a kit is useful for detecting a risk of cancer or polypeptide and a kit is useful for detecting a risk of cancer or polypeptide and a kit is useful for detecting a risk of cancer or polypeptide and transcript-derived nucleic acid samples and also in components and transcript-derived nucleic acid samples and also in microarrays. Sequences of PSP and PSNA are useful as hybridisting nucleic acids from both CC detabases for search analysis as well as in sequence analysis algorithms. PSNA is useful as components in cCC detabases for search analysis as well as in sequence analysis algorithms. PSNA is useful as pSNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide useful for diagnosing and monitoring the presence metastases of prostate cancer in a patient and as a component in databases for search analysis as well as in sequence analysis
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Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 other;

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Score 560; pred. No.

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RESULT 11
The present sequence is one of 3351 sequences in a library of human CC polynucleotides. The library is used to detect differentially expressed CC genes correlated with a cancerous state of a mammalian cell and can CC detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies CC of the polynucleotides. The probes can be used for chromosome mapping of CC the polynucleotide and for detection of transcription levels. Ribozymes CC or antisense oligonucleotides can be generated. The polynucleotides and CC their gene products are used as genetic or biochemical markers (e.g. in CC blood or tissues) that will detect the earliest changes along the CC carcinogenesis pathway and/or monitor the efficacy of therapies and CC preventive interventions. The polynucleotides, polypeptides and CC preventive interventions are used in pharmaceutical compositions to CC treat the cancers and proliferative disorders such as neoplasia,
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Reinhard C, R
Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                Library of polynucleotides for diagnosing a cancerous state mammalian cell and detecting cancer, particularly of the col prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                   Claim
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02-JUL-1999;
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(HYSE-) HYSEQ 1
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cancer; lun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia V,
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Randazzo F,
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99US-0142311.
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g cancer; cancer detection; s
                                                                                                                                                                                                                                                                                                               1046pp; English.
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Dickson M,
LW, Strache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Innis MA,
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umson G, Drm
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Best Local S
Matches 401
                                                                                                                                                       25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI59654 standard; cDNA; 1069
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                                            (HYSE-)
                                                                                                               14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                     2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0693036.
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Matches 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constance.
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P-PSDB; AAM40498.
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The sequence data for this patent did not form part of the printed
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Goodrich
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CC toxicological response to an agent, which comprises comparing a cypression profile of one or more human toxic response genes to a certaining the presence of a toxic response to the agent. Also catetarning the presence of a toxic response to the agent. Also catetarning the presence of a toxic response to the agent. Also catetarning the presence of a toxic response to the agent. Also catetarning the presence of a toxic response to the agent. Also catetarning the presence of a toxic response to the agent. Also catetarning the partial sequences given in ABS82842 (crown the genes corresponding to the partial sequences given in ABS82842 (crown toxic response gene plays a role on toxic response pathways by catetarning the expression profile of the gene after exposure of cells comprising: (a) exposing cells to an agent or isolating cells from a comprising: (a) exposing cells to an agent or isolating the test gene catetarning the test gene comprising the test profile to the expression profile of a similar function or comparing the test profile to the expression profile of a gene with crown continuous are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human compounds and chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxicologically relevant human nucleotide sequence
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RESULT 14
ABK12143/c
ID ABK12143 standard; cDNA; 693 BP
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AC ABK12143;
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DT 05-JUN-2002 (first entry)
XX
DT 05-JUN-1 homologous sequenc
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KW Human MIVR-1 homologous sequenc
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KW Cytostatic; cardiant; cerebropr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
  Disclosure;
                      Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
                                                        WPI; 2002-280912/32
                                                                               Lee
                                                                                                                                      22-AUG-2000; 2000US-227159P
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                                                                              Landschulz KT,
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  Page 101;
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Pred. No. 1.7e-15
D; Mismatches
  English
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RESULT 15
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Best Local (
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                                                                                                   DE19820190-A1
                                                                                                                                                                                                                      Human prostate
                                 28-APR-1998;
                                                                   04-NOV-1999.
                                                                                                                                                                     treatment;
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                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAX52885-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-621386/54.
P-PSDB; AAY74135, AAY74136, AAY74137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 269-270; 502pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nucleic acid sequences from pancreatic tumors, and related
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Search completed: August 27, 2003, 21:42:01 Job time : 421 secs

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ALIGNMENTS

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			COMMENT	JOURNAL	AUTHORS	REFERENCE		ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 BM922276
clone distribution: McC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12791 row: n column: 06 High quality sequence stop: 671.	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation	Email: cgapbs-r@mail.nlh.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc.	Contact: Robert Strausberg, Ph.D.	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 1046)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	EST.	BM922276.1 GI:19372655	5', mRNA sequence. BM922276	AGENCOURT_6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437	

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/mol_type="mRNA"
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Pred. No. 1.7e-269;
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BQ641849.1 GI:21
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AGENCOURT_8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCWA493 row: g column: 18
High quality sequence stop: 571.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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1 (bases 1 to 967)
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                                                                ACAGTGTCAGGCAACGGAATCCCAGAGCCGCGAGGTCTACGCCCCGCCTCGGCCCACCGAC
CGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT
                                            ACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-d7 priming. Directionally cloned into EcoRi/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
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/clissue_type="normal pigmented retinal epithelium"
/lab_host="DHIOB (phage-resistant)"
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/db_xref="taxon:9606"
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Pred. No. 1.7e-261;
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AGENCOURT_8825282 I
IMAGE:6204609 5', n
BQ954555
BQ954555.1 GI:2237
EST.
                                                                                                                                                                Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM13626 row: c column: 10

High quality sequence stop: 669.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                 Unpublished
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/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="pH10B"
/clone_lib="Lupski_sciatic_nerve"
/clone_lib="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit/Not1; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
                                                                                                                                                        Location/Qualifiers
                                                                                     /sex="male"
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5'-GACTAGTTCTAGATCCCGAGGGGCCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
354 c 273 g 127 t
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Pred. No. 4.3e-241;
0; Mismatches 2;
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cDNA (Un
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pp mRNA linear EST 15-
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Email: graeme@hellx.nih.gov
Plate: 13 row: h column: 06
Seq primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), (2002) In press Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               AGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGA 930
                                                                                                                                                     CCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCACCACCATCTCGCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100g of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGACCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd13h06"
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/dev_stage="Adult"
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1051 CATCAGCGCCACGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCCACCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity A
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                                                                                                                                                                                                                                                                                                                                                                                                                                           consortium, for clone orders contact:
Seq primer: -40RP from Gibco
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Homo sapiens
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, Jackson,Y. and Bowers,Y.
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Location/Qualifiers
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/note-"Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column
                                                                                                                                                             /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:5677341"
                                                                                                            /clone_lib="Melton Normalized Human Islet 4 N4-HIS
                                                                                                                                                                                                                       /sex="Both"
                                                                                                                                         /lab_host-"DH10B"
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          1 (bases 1 to 951)
Li,W.B., Gruber,C.,
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                         951 bp mRNA linear EST 31-MAY-200: sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED CDNA clone CSODJ015YF12 3-PRIME, mRNA sequence.
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Matches 733;
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cg1-bin/Cluster.cg1?seq=CSODJ015DC06NP1&cluster=9945.r. C
gen Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSODJ015DC06NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence clusy945.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de S
BP 191 91006 EVRY cedex - France
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/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
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/clone="CS0DJ015YF12"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Loases 1 to 729)
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BQ575741.1 GI:21479058
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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POLYA-Yes
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primer: M13 FORWARD
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//lab.host-"DHIDB (Life Technologies)"
//lab.host-"DHIDB (Life Technologies)"
//clone_lib-"NCI_CGAP_Ch2"
//note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: pT7T3-Pac (Pharmacia)
//note="
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ur-H-EZI-bbg-h-14-0-UI"
/tissue_type="Chondrosarcoma Grade
/dev_stage="Adult"
                                                             TAG_LIB-UI-H-EZ1
TAG_TISSUE-grade-2-chondrosarcoma
TAG_SEQ-ATCTAATATG"
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                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 850)
High quality sequence stop: 499
Location/Qualifiers
                                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM2679 row: 1 column: 22
                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         Unpublished
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National Institutes of Health, N
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/clone="IMAGE:6497853"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
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Tissue Procurement: ATCC
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                                   ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6209341"
/clone="pe="ductal carcinoma, cell/lab_host="pH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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AGENCOURT_10186171 NIH_MGC_101 Homo
IMAGE:6537543 5', mRNA sequence.
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National Institutes of Health, Mammalian
Unpublished
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1068)
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http://image.llnl.gov
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CDNA Library Arrayed by: The LOS. G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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                                      Score 471; DB 13;
Pred. No. 4.5e-198;
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Catarrhini; Hominidae;
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NHH_MGC_110"
/clone_lib="NHH_MGC_110"
/note="organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed
                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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0 Homo sapiens
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AGENCOURT_10442713 NIH_MGC_107 Homo
IMAGE:6650839 5', mRNA sequence.
BU859860
                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                        1 (bases 1 to 964)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2896 row: 1 column: 07
                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                              cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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Note: this is a NIH_MGC Library."
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AGENCOURT_10215265 NIH_MGC_107 H
IMAGE:6569922 5', mRNA sequence.
BU539219
               Unpublished
Contact: Robert Strausberg,
                                                                                                                                                               BU539219.1 GI:22849660
EST.
                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                               Homo sapiens
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cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: breast; Vector: pOTB7; Site_1: ECORI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_107"
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Catarrhini; Hominidae,
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cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2757 row: p column: 18
High quality sequence stop: 663.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGGGGGGGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA 267
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                                                                  AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 100
                                                                                                                                                                                                                                                                                                                                                   ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCT 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: breast; Vector: pOTB7; Site_1: EcoR1; Site_2: XhoI; cDNA made by oligo-dT priming: Site_2: XhoI; cDNA made by oligo-dT priming: Sites using the Directionally cloned into EcoRi/XhoI sites using the following 5 adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library. 1 others
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/clone_11b="NIH_MGC_107"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="adenocarcinoma, cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone-"IMAGE: 6569922"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 449; DB 13;
pred. No. 2.6e-188;
0; Mismatches 4;
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BQ015170/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 782)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iow

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ015170.1 GI:19740071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: M13 FORWARD
                                                                                                                                                                                                                                                                   109
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                    (Pharmacia) with a modified polylinker; Site_1: Ecor I; (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP_ED] is a normalized cDNA library containing the following tissue(s): Chondrosarcoma cell line CS5. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and coloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is sequence tag for this library tag sequence that is sequence tag for this library is GCTCAAGGCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5834635"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
                                                                                                                                                                                                                                                               TAG_TISSUE-chondrosarcoma
TAG_SEQ-CGTCAAGGCT"
223 c 271 g 176
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/db_xref="taxon:9606"
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/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
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                                                                                                                                                             Score 445; DB 12;
Pred. No. 1.6e-186;
0; Mismatches 2;
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RESULT 15
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                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 602) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA431191.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
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                                                                                                                                                                                                                                                                                           Seq primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
/organism="Homo sapiens"
/mol_type="nRNA"
/db_xref="taxon:9606"
/clone="UI-H-FGI-bgi-c-12-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="%CI_CGAP_FGI"
/note="Organ: Enchondroma; Vector: pT7T3-Pac (P)
with a modified polylinker; Site_1: EcoR I; Site
                                                                                                                                                                                                                                                Location/Qualifiers
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CDNA clone
         c (Pharmacia)
Site_2: Not
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                                                                   CAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGCCGGGCCTGG
                                                                                                                             GGCTGCGTAGGTGAAAAGGCAG 1321
                                         CAAAGAGAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCCCCAGGGGGGGCCGGGCTGG
                                                                                                                                                                         CGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCT 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_SEQ-CGGTCACTC"
179 c 196 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James Martin from the University of Iowa. TAG_LIB-UI-H-FG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
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Pred. No. 3.4e-185;
); Mismatches 0;
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Search completed: August 27, time : 3117 secs

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182

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-286-010-1
US-07-775-490-1
US-07-771-891B-1
US-08-455-073A-1
US-08-455-073A-1
US-08-455-25-5
US-09-286-25-5
US-09-286-25-5
US-09-286-27-7-25-3
US-09-780-173A-10
US-08-819-177-2
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US-08-819-177-2
US-08-357-251-3
US-09-377-66A-7
US-08-312-766A-7
US-08-312-866-1
US-09-310-838-249
US-09-310-838-249
US-09-288-986-42
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3 US-07-827-691A-4	US-09-497-933A-20	US-09-497-933A-24	US-08-484-408A-32	US-08-484-408A-31	US-08-480-173A-32	US-08-480-173A-31	US-09-497-933A-25	US-09-497-933A-23	US-09-497-933A-18	US-09-497-933A-21	US-09-497-933A-19	US-09-497-933A-22	US-08-068-747-7	US-08-068-747-2	FCT-US93-06828-3	2 US-08-775-607-3	US-08-775-609-3
Sequence 4, Appli	Sequence 20, Appl	Sequence 24, Appl	Sequence 32, Appl	•	Sequence 32, Appl	•	Sequence 25, Appl	Sequence 23, Appl	Sequence 18, Appl	•	Sequence 19, Appl	Sequence 22, Appl	Sequence 7, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli

ALIGNMENTS

APPLICANT: SEGANA, TAKEHIKO APPLICANT: SEGANA, TAKEHIKO TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED TITLE OF INVENTION: POYNOCLEOTIDE ARRAY FILE REFERENCE: 04995.0057-00000 CUGRENT APPLICATION NUMBER: US/09/769,482 CUGRENT FILING DATE: 2001-01-26 PRIOR APPLICATION NUMBER: 60/178,772 PRIOR APPLICATION NUMBER: 60/179,045 PRIOR FILING DATE: 2000-01-31 NUMBER OF SEQ ID NOS: 67 SOOTWARE: PATENTIN VET. 2.1 SEQ ID NO 1 LENGTH: 1140 TYPE: DNA ORGANISM: Homo sapiens ; NAME/KEY: CDS ; LOCATION: (95)..(850) US-09-769-482-1 US-09-769-482-1 Sequence 1, Application US/09769482 Patent No. 6566130 GENERAL INFORMATION: Query Match Best Local Similarity APPLICANT: SRIVASTAVA, APPLICANT: MOUL, JUDD FEATURE: 60.6%; Σ Score 800; Pred. No. DB 4; Length 1140;

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762 279 702

ACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACCT

GCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGTCTACGCCCCGCCCTCGGCCCACCG

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GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG

219 642 159

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Matches 800;

Conservative

0,

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522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGG

CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATGATGGTGATGGTGG

582 TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA

TGATCACGTGCCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA

GCCAGGGGCGGAGAGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGA

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
APPLICANT: SEGAWA, TAKEHIKO
PLICANT: SEGAWA, TAKEHIKO
PLICANT: SEGAWA, TAKEHIKO
ITLE OF INVENTION: POYNICLECTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT APPLICATION NUMBER: 50/178,772
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTMARE: PATENTIN VET: 2.1
SEQ ID NO 2
LENGTH: 759
TYPE: DNA
ORGANISM: Homo sapiens
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                                                      Similarity
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 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGG
                                          Conservative
                                           57.2%; Score 755; DB 4; L
100.0%; Pred. No. 1.7e-313;
Live 0; Mismatches 0;
                                                               Length 759
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US-09-236-097-7
                                                                                                                                                                                                            Sequence 7, Application US/09236097 Patent No. 6335165
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                              STREET: 20001 Je
CITY: Arlington
STATE: Virginia
COUNTRY: United
ZIP: 22202
                                                                                                                                   ADDRESSEE:
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                                                                                        United States
                                                                                            of.
                                                                                            America
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GENERAL INFORMATION:

APPLICANT: -NIR NAVOT ET AL

TITLE OF INVENTION: METHODS AND KITS FOR CHARACTERIZING
TITLE OF INVENTION: -RICH NUCLEIC ACID SEQUENCES

NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" micr.
COMPUTER: Twinhead* 5limnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.1
SOFTWARE: Word for Windows version 2.2
SOFTWARE: an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 TGATCACGTGCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA
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                                                                                                                                                              E: Mark M. Friedman c/o Anthony
20001 Jefferson Davis Highway,
                                                                            5" microdisk
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                                                                                                                                                                 Castorina Suite 207
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RESULT 4
US-09-086-010-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Glimch
                                             REFERENCE/DOCKET NUMBER: HUI-027CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/
FILING DATE: 2-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33 883
REFERENCE/DOCKET NUMBER: 12/
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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APPLICATION NUMBER: US
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                               NAME: Kara, Catherine J. REGISTRATION NUMBER: 41,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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 STRANDEDNESS:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/086,010
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 GGCGGCGGCGGCGGCGGAGGCG 532
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               : 1203 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glimcher, Laurie H. et al. VENTION: Human c-Maf Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
single
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; ANTI-SENSE: 1
US-07-705-490-1
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US-07-705-490-1
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RESULT 6
US-07-751-891B-1
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                                                                                                              Matches
                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07, FILING DATE: 19910708 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Paul, Thomas D. REGISTRATION NUMBER: 32,7;
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Warren, APPLICANT: Oostra, TITLE OF INVENTION:
                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
                                                                                                                                                                                                                                                                                                            TELEPHONE: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 77010-3095
                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         TELEFAX: 713/
TELEX: 762829
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                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                  ENGTH:
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                                                                                 56 GGCGGCGGCGGCGGCGGAGGCG 83
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                                                       44 GGCGGCGGCGGCGGCGGCGGAGGCG 71
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                                                                                                                                                                                                                                                               3765 base pairs
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Oostra, Ben A.
                                                                                                            Conservative
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Nelson, David L.
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                                                                                                                                                                                                                                                                                                                                                                            32,714
                                                                                                                        Score 28; DB 3; Pred. No. 0.0052
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; Pred. No. 0.0059;
                                                                                                            0;
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                                                                                                            Mismatches
                                                                                                                                     Length 3765;
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Sequence 1, Application US/07751891B Patent No. 6180337

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RESULT 7
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                                                                                                                                                                                                          Patent No. 5876949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ery Match
                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                              APPLICANT: Gideon Dreytuss
APPLICANT: Mikiko C. Siomi
APPLICANT: Yan Zhang
                                                                                                          TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Caskey, C. T.
Nelson, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
                                          ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. STREET: One Liberty Place, 46th floor
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                              44 GGCGGCGGCGGCGGCGGCGGAGGCG 71
                                                                                                                                                                                                                                                                                                                                                56 GGCGGCGGCGGCGGCGGAGGCG 83
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28; Conservative
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                              Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 762829
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                                                                                                                                                                                                                              Application US/08455073A
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                                                                                                                                                                              Gideon Dreyfuss
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paul
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  ; DB 3; L. do. 0.0052; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3765;
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US-08-455-073A-1
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US-08-457-273B-41/c
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REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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Sequence 41, ner-
S849995
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
ANAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Mouse Model for Huntington's Disease and TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
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Local Similarity 100.0%;
les 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                  STREET: PO Box 3/428
CITY: Rale1gh
STATE: No. 5849995th Carolina
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                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayden, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nasir, Jamal
                                                                                                                                                                                                                                                                                         SD
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31-MAY-1995
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PC-DOS/MS-DOS
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; Pred. No. 0.0051
0; Mismatches
                                                         3477-85A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-556-419-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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SEQ ID NO 13
LENGTH: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                         09-041-886-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equence 13, Apprint No. 6093549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSS,
APPLICANT: Li, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                           quence 14, Application US/09041886
tent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Worley, Paul
PPLICANT: Snyder, Solomon
ITLE OF INVENTION: Huntingtin-associated protein
ILE REFERENCE: 01107.52271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pai
CURRENT APPLICATION DATA:
                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                        COUNTRY:
                                                                                                                                                     STREET:
                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       469 GAGGAGGCGGCGGCGGCGGCGGCGG 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                     San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NOS: 25
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharp, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lanahan, Anthony
                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08556419C
                                                                                                                                                    E: Campbell & Flores LLP 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Shi-Hua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 28; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
                                                                                                        United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xiao-Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                 Peptides, Dependence and Methods of Use
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. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
. 0.0047;
                                                                                                                                                     Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pairs
TYPE: nucleic acid
                                                                                                          TELEFAX: (202) 371-25 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08, FILING DATE: May 20, 1994 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MacDonald, Marcy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC comparing
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      NAME: Goldstein, Jorge, A. REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New CITY: Washington
                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
NAME/KEY:
                            TOPOLOGY:
                                                                                                                                      TELEPHONE:
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                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GAGGAGGCGGCGGCGGCGGCGGCGG 78
                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sterne, Kessler, (
                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                      (202) 371-26
(202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duyao, Mabel P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ambrose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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316..9748
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                                         single
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                                                                                                                                          371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Christine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 28; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                   US/08/246,982A
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. 0.0047;
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; LOCATION: US-08-246-982A-5

316..9748

Best Local Similarity 100.0%; Matches 28; Conservative

Score 28; DB 1; pred. No. 0.0047;

Length 10366;

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Mismatches

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Indels

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Gaps

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RESULT 12 US-08-453-265-5/c

Patent No. 5693757

Application US/08453265

GENERAL INFORMATION:

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51 GAGGAGGCGGCGGCGGCGGCGGCGG 78

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; NAME/KEY:
; LOCATION:
US-08-453-265-5
                                                                         RESULT 13
US-09-325-932A-2/c
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                             ; GENERAL INFORMATION:
                                            sequence 2, Application US/09325932A
Patent No. 6451604
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-25
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                          469 GAGGAGGCGGCGGCGGCGGCGGCGG
                                                                                                                                                                    51 GAGGAGGCGGCGGCGGCGGCGGCGG 78
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1100 New York Avenue
   Lasham,
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Pred. No.
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0.0047;
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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 367
TYPE: DAN
ORGANISM: Pinus radiata
US-09-325-932A-2
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US-09-780-173A-10
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; NAME/KEY: CDS
; LOCATION: (344)...(1396)
US-09-780-173A-10
                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-819-177-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
TITLE OF INVENTIONS ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.0%;
Best Local Similarity 100.0%;
Matches 26; Conservative
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TITLE OF INVENTION:
FILE REFERENCE: 102:
                                                                                                                                                                                                                                                                                  Sequence 2, Applic
Patent No. 6043083
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.0%; Score 26; Best Local Similarity 100.0%; Pred. No. Matches 26; Conservative 0; Mismatcl
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LENGTH: 1877
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CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                              APPLICANT: Davis, Roger J.
APPLICANT: Dickens, Martin
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAY AND MET
             COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                   CITY: Boston
STATE: MA
                                                                                                        ADDRESSEE: Fish a .-- street street: 225 Franklin Street
COMPUTER:
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IBM Compatible
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
INFORMATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/819,177
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/037001
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2832 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
YMAME/KEY: Coding Sequence
LOCATION: 180...2159
OTHER INFORMATION: JIP-1 cDNA
US-08-819-177-2

2.0%: SCOTE 26; DB
Search completed: August 27, 2003, 23:59:59 Job time: 100 secs
                                                                                                                                                             Query Match 2.0%; Score 26; DB 3; Length 2832; Best Local Similarity 100.0%; Pred. No. 0.038; Matches 26; Conservative 0; Mismatches 0; Indels
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Perfect score:
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length: 2000000000
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Gapop 60.0 , Gapext 60.0
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Match
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1321
1 cgaccgcggtctcggagcga.....ctgcgtaggtgaaaaggcag 1321
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/cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USIO_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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                              US-09-934-249-1
US-10-241-220-119
US-09-934-249-3
US-10-301-822-208
US-10-205-823-412
US-10-205-823-412
US-10-205-823-412
US-10-098-841-71
US-09-796-753-55
US-10-241-220-45
US-10-200-256A-32
US-09-918-995-2074
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US-09-783-590-3468
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sequence
                                                                                                                                                                                                                                                           Sequence
   3, Appli
208, App
412, Appl
44, Appl
71, Appl
55, Appl
55, Appl
32, Appl
12, Appl
2074, Appl
3464, Ap
3464, Ap
3484, Appl
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US-10-098-841-280	-381	US-10-177-293-285	-09-920	US-10-144-649A-418	US-09-854-133-418	US-09-738-973-418	-455-	-879-312-	-10-215-432-	-165-		-10-215-432	us-09-783-590-3813		US-10-060-036-418	US-10-215-432-29	US-10-017-621-89	US-10-177-293-42	US-09-905-983-45	US-09-836-960-4	US-10-062-254-279	US-09-836-960-1	US-09-864-761-20699	US-09-864-761-3936	61-3	US-10-259-165-327	US-09-864-761-20542	US-09-934-249-15
`	'n	285		418,	418,	418, /	211		26, 1	762,		30,	381	13163	418,	29,	, 68	e 42	5,		27	e 1, App	206	Sequence 3936, Ap	3776,	Sequence 327, App	20542	Sequence 15, Appl

ALIGNMENTS

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; NAME/KEY: CDS
; LOCATION: (413)...(1273)
US-09-934-249-1
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
APPLICATE Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
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LENGTH: 1321
TYPE: DNA
ORGANISM: HOMO S
FEATURE:
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APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Ratherine
APPLICANT: Turi, Thomas G.
                                                                                                                                                 Query Match
Best Local Similarity 100
Matches 1321; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09934249 Patent No. US20020115081A1
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
   61
                 61 CGGCGGCGGCGGCGGGGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCCTCAGCCCC
                                                                                             1 CGACCGCGGTCTCGGAGCGAAACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGAGGCGG
CGGCGGCGGCGGCGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCAGCCCC
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                                   GCGCATGGAGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTC
                                                                                                                                                                                   GATCGACCTGCCACCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGG
                                                                                                                                                                                                                      CTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGA
                                                                                                                                                                                                                                                                                                                                           GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCA 540
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: .2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-119
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Best Local s
Matches 1229
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Phillips, Heidi
Polakis, Paul
Spencer, Susan
Williams, P. Mickey
Wu, Thomas
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US20030148408A1
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GENERAL INFORMATION:

APPLICANT: Lee, Richard T.

APPLICANT: Landschulz, Katherine T.

APPLICANT: Turi, Thomas G.

APPLICANT: Thompson, John F.

APPLICANT: Thompson, John F.

APPLICANT: Kennedy, Scott P.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS

FILL REFERENCE: P0738/7001/EFP/KA

CURRENT APPLICATION NUMBER: US/09/934,249

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/227,159

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FASTSEQ for Windows Version 3.0
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Patent No. US20020115081A1
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LENGTH: 861
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Murgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-05-20
PRIOR PILING DATE: 2002-05-20
PRIOR PILING DATE: 2002-05-20
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US-10-301-822-208
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US-10-301-822-208
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
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Best Local Similarity
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AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 100:
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                                                                                             AGCCCCACCCTACCAGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG 941
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                                                                          AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG
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b. US20030148410A1
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; TYPE: DNA
; ORGANISM: Homo s
US-10-205-823-412
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PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-13
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                             Matches
                                                                           Query Match
Best Local
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSI
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
FULL REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR ETLING DATE: 2001-07-25
PRIOR ETLING DATE: 2001-07-25
PRIOR ETLING DATE: 2001-07-25
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                                                                                                                                                                                                      NUMBER OF SEQ ID SOFTWARE: FastSEQ
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/362,158 PRIOR FILING DATE: 2002-03-05
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Kamatkar, Shubhangi
Wonsey, Angela M.
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Gorbatcheva, Bella
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Endege, Wilson O.
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LSEQ for Windows Version
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Sequence 44, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
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US-10-241-220-44
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: COMPOSITIONS AND METH
TITLE OF INVENTION: TERATMENT OF TUMOR-
FILE REFERENCE: P5010R1-US
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
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Sequence 71, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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Best Local S
Matches 800
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TYPE: DNA
ORGANISM:
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; LOCATION: (154)..(867)
US-10-098-841-71
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CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
VRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
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SEQ ID NO 71
LENGTH: 1066
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Best Local Similarity 100.0%;
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APPLICANT: Qian, Xiaohong B.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1el Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
        1014
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      GGCTGGGCGGCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCA 1073
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Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
                                          AGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGATGGATAGTGCCA
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Wehrman, Tom
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Wang, Dunrui
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Xu, Chongjun
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Pred. No.
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-12
PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER:
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
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TITLE OF INVENTION:
                                                                                                                                                                                                             OR APPLICATION NUMBER: 09/22
OR APPLICATION NUMBER: 09/22
OR FILING DATE: 1998-12-30
OR APPLICATION NUMBER: 09/25
OR FILING DATE: 1998-02-26
OR FILING DATE: 1999-03-01
OR APPLICATION NUMBER: 09/25
OR FILING DATE: 1999-03-01
OR APPLICATION NUMBER: 09/31
OR FILING DATE: 1999-05-14
OR APPLICATION NUMBER: 09/33
OR FILING DATE: 1999-06-18
OR APPLICATION NUMBER: 09/33
OR FILING DATE: 1999-06-29
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OR FILING DATE: 1999-06-30
OR APPLICATION NUMBER: 09/36
OR FILING DATE: 1999-07-30
OR APPLICATION NUMBER: 09/36
OR FILING DATE: 1999-09-20
OR APPLICATION NUMBER: 09/36
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OR FILING DATE: 1999-09-30
OR APPLICATION NUMBER: 09/36
OR APPLICATION NUMBER: 09/37
OR APPLICATION NUMBER: 09/37
OR APPLICATION NUMBER: 09/37
R FILING DATE: 2000-02
R APPLICATION NUMBER:
R FILING DATE: 2000-05
R APPLICATION NUMBER:
R FILING DATE: 2000-05
R APPLICATION NUMBER:
                                                                                                                                                      APPLICATION NUMBER: 09/474,071
FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/474,072
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                                                                                                                                      FILING DATE:
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IVENTION: SECRETED PROTEINS

INCE: 7853-227-999
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PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-29
PRIOR PPLICATION NUMBER: 09/630,334
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-07-31
PRIOR PRICING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR APPLICATION NUMBER: 09/606,366
PRIOR APPLICATION NUMBER: 09/655,666
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
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Best Local
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LENGTH: 969
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ORGANISM: Homo
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LOCATION: (6)...(761)
9-796-753-55
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                1182
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                                                           GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG
                                                                                                                     CGTGCTACGGCAGCGGCGGGCGCATGGAGGGGCCGCCGCCCCACCTACAGCGAGGTCATCG
                                                                                                                                                                              TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCA 1061
                                                                                                                                                                                                                                        AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA
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; SEQ ID NO 45
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo St
US-10-241-220-45
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Best Local S
Matches 763
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APPLICANT: Williams, P.Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
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                          AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
                                                                                     AGCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGG
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Spencer, Susan
Williams, P. Mickey
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99.9%;
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Pred. No. 0;
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sel-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to
TITLE OF INVENTION: MADER: US/10/000,256A
CURRENT APPLICATION NUMBER: 0001-11-01
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION UNMBER: 60/244,782
PRIOR APPLICATION UNMBER: 60/244,782
PRIOR APPLICATION UNMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
SEQ ID NO 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 1583
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; ORGANISM: Homo sapien
US-10-000-256A-32
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                                                      GGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGGTCCTCCTTCCAGCA 1149
Length 1583;
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APPLICANT: Kennedy, Scott P.
APPLICANT: Kennedy, Scott P.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
TITLE REFERENCE: P0738/7001/ERP/RA
FILE REFERENCE: P0738/7001/ERP/RA
FILE REFERENCE: P0738/7001/ERP/RA
FILE REPELICATION NUMBER: US/09/934,249
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT EPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEG ID NOS: 17
SEG ID NO 14
SEG ID NO 14
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TYPE: DNA
TYPE: DNA
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FEATURE:
NAME/KEY: unsure
LOCATION: (639)...(639)
OTHER INFORMATION: a, C, 9
US-09-934-249-14
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Matches 302
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APPLICANT: Landschulz, Katherine
APPLICANT: Turn, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
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                                                                                                                                                                                                                           | GG 1186
                                                                                                                                                  ACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGCAGG 1184
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ilarity 100.0%; Pred. No. 8.6e-13;
Conservative 0; Mismatches 0;
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LOCATION: (1)...(467)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-783-590-3464
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US-09-918-995-2074
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Best Local
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                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. SEQ ID NO 3464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR ETLING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, Willia
                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
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                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                     NAME/KEY: misc feature
LOCATION: (103)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                  TYPE: DNA
NAME/KEY: misc feature
LOCATION: (225)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                         LENGTH: 368
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Similarity 100.0%; Pred. No. 1.7e-76;
78; Conservative 0; Mismatches 0;
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Best Local :
                                                                    Matches
                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1995-04 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16 FILE REFERENCE: PO-16.2C1
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/420,856
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APPLICANT: Haseltine, Willia
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                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (51)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (367)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                            FEATURE:
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                                                                                     Local Similarity
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              1187 ACCCGGCTCCACCACACACACATCGCGCCCCTAGAGAGCGCA 1228
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TACCCGGGGTCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCCTCCTT
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0020110850A1
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                                                                    Conservative
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                                                                                   100.0%;
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US-09-934-249-12
US-09-934-249-12
Sequence 12, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lede, Richard T.
APPLICANT: Tandschulz, Katherine T.
APPLICANT: Tionpson, John F.
APPLICANT: Kennedy, Scott P.
APPLICANTION: CARDIOVASCULAR CONDITIONS
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
FILER REFERENCE: P0738/7
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Search completed: August 28, 2003, 01:25:41 Job time: 372 secs
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Listing first 45 summaries
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gb_ph:*
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TITLE

Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G. Diagnosis and treatment of cardiovascular conditions

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AUTHORS	SOURCE ORGANISM	RESULT 1 AX392417 LOCUS DEFINITION ACCESSION VERSION VERSION		c 45 1	421		38 2			33 2			22 7			22		19			1 1 4 5 4	C 13 4	11			7 6		.		י	Result No. S	
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P., Thompson,	a; Vertebrata ini; Hominida	A linear																														
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      AGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGG
                                           GATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGGTGATCACGTGCCTGAG
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BRIGHAM AND WOMEN'S HOSPITAL, I
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YGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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                                                     Direct Submission
Submitted (14-SEP-2000)
                                     Queensland University
4001, Australia
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/organism="Homo sapiens"
/mol_type="mRNA"
                             Location/Qualifiers
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STAG1/PMEPA1 mRNA,
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Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A. Characterization of a novel gene, STAGL/PMEPA1, upr renal cell carcinoma and other solid tumors Mol. Carcinog. 32 (1), 44-53 (2001)
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YGSGGRHEGGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAPLESAAIWS
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consc
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Homo sapiens, clone MGC:20374
BC015918
BC015918.1 GI:1619847/
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hisiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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mmalia; Eutheria; Primates; Catarrhini; Hominidae;
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4 IMAGE:4559576, mRNA,
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M.A.G.E. Consortium
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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SDGEEPPPYGGCFCTLALRDESURLAWESURAFPHRRQPTYPLOSDLMDSARLGGFCPPSS
NSGISATCYGGSGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPPSLLEGTRLHHTHIAP
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/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
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Location/Qualifiers
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AF224278.1 GI:9255808
Xu,L.L., Shanmugam,N., Se
Moul,J.W. and Srivastava,
Direct Submission
Submitted (12-JAN-2000) C
                                                             A novel androgen-regulated gene, PMEI 20q13 exhibits high level expression Genomics 66 (3), 257-263 (2000)
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1141)
                                                                                        Xu,L.L., Shanmugam,N., Segav
Moul,J.W. and Srivastava,S.
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RRREDALSSEGCLMPSESTVSGNGIPEPQVYAPPRPTDRLAVPPFAQRERFHREQPTY
PYLQHELDLPPTISLSDGEEPPPYQGFCTLQLRDPEQQLELNRESVRAPPNRTITDSD
LMDSARLGGPCPPSSNSGISATCYGSGGRMEGPPPTYSEVIGHYPGSSFQHQQSSGPP
SILEGTRLHHTHIAPLESAATWSKEKDKQKGHPL"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
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/protein_id="AAF86322.1"
/db_xref="GI:9255809"
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1 (bases 1 to 1818)

1 (bases 1 to 1818)

Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E., Wilson, J.K., Lu, S., Nosrati, A., Rerko, R.M., Swinler, S., Beard, L., Willson, J.K., Lu, S., Nosrati, A., Rerko, R.M., Swinler, S., Beard, L., Willson, J.G., Willis, J., Platzer, P. and Markowitz, S. Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. tutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S. Beard, L., Patzer, P. and 
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                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUL-2002) Department of Medicine, Case Western Reserve University/Howard Hughes Medical Institute, 11001 Cedar Ave., Cleveland, OH 44106, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence Willson, J.K.V., Lu, S., Nosrati, A., Swinler, S., Beard, L., Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
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ilarity 100.0%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
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              Strausberg,R.
Direct Submission
Submitted (23-AUG-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                               Mus musculus
Eukaryota; Me
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13/9 DP mRNA linear ROD 26-SEP-20 Mus musculus, Similar to transmembrane, prostate androgen induced RNA, clone IMAGE:5038092, mRNA. ROD 26-SEP-2002

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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USA
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This clone was selected for full length: sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.
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Series: IRAK Plate: 81 Row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
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Contact: MGC help desk
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VVMMVMYVMITCLLSHYKLSARSFISHHSQARRRDDGLSSEGGCLWPSESTVSGGMPEP
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                     GPPPTYSEVIGHYPGSSFQHQQSNGPSSLLEGTRLHHSHIAPLENKEKEKQKGHPL*
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Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A. Identification and characterization of a novel gene, up-regulated in renal cell carcinoma and other solid
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Submitted (13-SEP-2000) Centre
Queensland University of Techno
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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,F.K., Hooper,J.D., Nicol,D.L.
                            CGGGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC
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/protein_id="AAL09357.1"

/db_xref="GI:15824469"

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YQGPCTLQLRDPEQQLELNRESYRAPPNRTIPDSDLMDSARLGGPPTSSNSGISATC
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join(321. .429,50206. .50360,56817. .56870,
/gene="STAGL/PMEPAL"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
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                                                                                                                                                                                                                                                                              Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre are unitable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerquest@sanger.ac.uk
on Dec 5, 2000 this sequence version replaced gi:10198628.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS718J7

130435 bp DNA linear PRI 24-FEB-200
Human DNA sequence from clone RP4-718J7 on chromosome
20q13.31-13.33 Contains the PCKI gene for soluble
phosphoenolpyruvate carboxykinase 1, part of a novel gene similar
to mouse DLM-1 (tumour stroma and activated macrophage protein),
the 3' end of the TMEPAI gene encoding an androgen induced 1b
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP4-718J7 The true end of clone RP5-1007E6 is at 71437 in this sequence. The true right end of clone RP4-579F20 is at 43945 in this sequence. RP4-718J7 is from the library RPCI-4 constructed by the group c Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; CpG island; DLM-1; macrophage protein; PCK1;
phosphoenolpyruvate carboxykinase; PMEPA1; TMEPAI;
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HTG; CpG island; DLM-1; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein (PMEPA1), two putative novel genes, a CpG island, ESTs, STSs and GSSs, complete sequence.
                                                                                                                      http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                      Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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2583. .2
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427. .
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/clone="RP4-718J7"
/note="AluJb repeat:
                   /note="AluJb repeat:
10263. .10573
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/mol_type-"genomic DNA"
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2346
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2718
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matches 1.
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one plasmid subclone or more than one M13 subclone; and assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 91. .218 of consensus"
6592. .6723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Charliel repeat: matches 681. .781 of consensus"
5331. .5793
                   /note="L2 repeat: matches 2292. .2511 of consensus"
10094. .10206
                                                                                                                          'note="MLT1D repeat: matches 105. .505 of consensus'
                                                                                                                                                                                                                                                                                               note="FLAM_C repeat: matches 1.
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2757
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                                                                                                                                                                  Alu repeat: matches 1. .34 of consensus"
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                                                                                   matches 1459.
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matches 188. .300 of consensus*
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.308 of consensus"

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note-"L2 repeat: matches 2647. .2749 of

11816. .12380

/note-"LTR19B repeat: matches 1. .580 of

12519. .12813
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                                                                                                                         25580. .25611
/note="16 copi
26333. .26643
                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 90. .143 of consensus" complement(21005. .21672) /note="match: GSS: Em:AQ748384" complement(21187. .21672) /note="match: GSS: Em:AQ776209" complement(21278. .21673) /note="match: GSS: Em:AQ136459" complement(21278. .21672) /note="match: GSS: Em:AQ136459" complement(21278. .21672) /note="match: GSS: Em:AQ136459" complement(21392. .21672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alux repeat: matches 1. 303 of consensus"
16333. .16396
16575. .16690
16575. repeat: matches 2596. .2711 of consensus'
18049. .18169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"10 copies 12 mer 82% conserved"
15028. .15111
/note-"14 copies 6 mer cacaca 82% conserved"
15029. .15108
/note-"20 copies 4 mer acac 83% conserved"
15273. .15399
/note-"12 repeat: matches 2159. .2285 of conserved"
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15026. .15109
/note="7 copies 12
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14313. .14437
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'note="L1MD2 repeat: matches 6032. .6331 of consensus"
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18312._.18438
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15015. .15110
/note="3 copies 32 mer 79% conservence"
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note="3 copies 56 mer 73% conserved"
                                                                                                                                                       /note="L2 repeat: matches 2336. 25580. .25611
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18585. .18776 -
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20413 . .20463
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"MER20 repeat: matches 7.
                                                                                                                                                                                       /note="2 copies 35 mer 100% conserved" 24257. .24591
                                               /note="MIR repeat:
                                                                             note="L2 repeat: matches 2661.
note="FLAM_C repeat: matches 1. .127 of consensus"
%1203. .31356
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8. .13715
                                                                                                                                                                                                                               ce="MIR repeat:
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                                                                                                        e-"AluY repeat: matches 1. .310 of consensus"
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Sequence 32 from Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0242776-A 32 30-MAY-2002; Diadexus, Inc. (US)
                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins
                                                             Sun,Y., Recipon,H., Chen,S.Y. and Liu,C.
                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                             CACACACACATOGOGOCOCTAGAGAGGGCAGCCATOTGGAGCAAAGAGAAGGATAAACA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGCGCATGGAGGGGCCGCCCCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTC
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nilarity 99.0%;
Conservative
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                     Location/Qualifiers
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1e-74;
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                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                        Human DNA sequence from clone RPS-10517 on chromosome 20q13.2-13.33 Contains the 5' end of the TMEPAI (PMEPAI) encoding an androgen induced 1b transmembrane protein, ES GSSs and two CpG islands, complete sequence.
ALL121913
ALL121913 4 GI:7161781
HTG: CpG island; PMEPAI; TMEPAI; transmembrane protein.
Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 6, 2000 this sequence version replaced gi:7007305.
During sequence assembly data is compared from overlapping clon where differences are found these are annotated as variations
                                                                                                         Skuce, C
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 150224)
                                                                                                                                                                  Homo
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This sequence is the entire insert of clone RP5-1059L7 The true
This sequence is the entire insert of clone RP5-1059L7 The true
left end of clone RP11-40ZP1 is at 106677 in this sequence. This
sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP5-1059L7 is from
the base of the constructed by the group of Pleter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further details see
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                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
/product="dJ105917.1.2 (androgen
transmembrane protein (PMEPA1), i
/protein_id="CAC32857.1"
/db_xref="GI:13160408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein (PMEPA1),
/note="match: cDNAs: Em:AF224278
match: ESTs: Em:AA088767"
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                               /evidence=not_experimental
complement(join(<2445. .2599,
/gene="TMEPAI"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(<2445. .2599,53362. .53365))
/gene="TMEPAI"
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/gene="TMEPAI"</pre>
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complement(2445. .53425)
                                                                                                                   Em: AA088767"
                                                                                                                                                                                                           transmembrane protein (PMEPA1), isoform 1)"
/note="match: cDNAs: Em:AF009426 Em:AF009427 Em:AF009425
                                                                                                                                                                                                                                                                                                                               complement(join(<2445. .2599,52376. .52477))
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/clone_lib="RPCI-5"
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/note="continues in dJ718J7 (AL035541)
                                                                                                                                                                                  Em: AF009424
                                                                                                                                                                                                                                              /product="dJ1059L7.1.1 (androgen induced type transmembrane protein (PMEPA1), isoform 1)"
                                                                                                                                                                                                                                                                                                      /gene="TMEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="dJ1059L7.1.2 (androgen induced type transmembrane protein (PMEPA1), isoform 2)
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                                                                                                                                                      Em: AA249792 Em: AI594390
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3473. . .
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VVMMVMVVVITCLLSHYKLSARSFISRHSQGRRREDALSS"
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/codon_start=1
/evidence-not_experimental
/product="dJ1059L7.1.1 (androgen indu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8103 . 8205
/note="MIR repeat: matches 48.
complement(8858 . 9277)
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3128. .3606
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/protein_id="CAB88144.1"
/db_xref="GI:7619746"
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                                                                                                                                                                                            14448. .14493
/note="23 copies 2 mer at 76% conserved"
14634. .14813
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                                          16989
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15096. .15497
                                                                                                                                                                                                                                                         12054. .12362
/note="AluSx_repeat: matches l.
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11630. .12037
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)224. .9382
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5002. .5190
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    /note="MLT1A2 repeat: matches
17647. .17703
                                                                                     /evidence=not_experimental
15690. .15935
                                                                                                                                                                                                                                                                                                                                                                                            note="Charlie4 repeat: matches 39.
                                                              'note="MIR repeat: matches 7.
                                                                                                                                'note="CpG island"
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4069
-"19 copies 2 mer tt 81% conserved"
5001
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3932
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3892
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ein (PMEPA1), isoform 1)"
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                                                                                                                                                                                                                                                                                                                                                   matches 11.
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                                                                                              39.6%;
nilarity 99.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"L2 repeat: matches 2679. 117699. .18179 /note-"match: GSS: Em:AQ703107" 17902. .18039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 61.
26450. .26485
/note="18 copies 2 mer tg 97% of the copies 2 mer tg 97% 
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note="MIR repeat: matches 35. .

19954. .20005

note="12 repeat: matches 2358.
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24460. .24580
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/note="MIR_repeat:
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1980. .22192
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3439. .23512
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.25042
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Pred. No. 1.3e-64;
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156
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Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, IN
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14
Ax392430
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                                                                                                                                                                                                                                                                                             CACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTAC
                                 TCCTCCTTCCAGCACCAGCAGCAGTGGGCCGCCCTCCTTGCTGGA-GGGGACCCGGCT
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                                                                     GGCGGGCGCATGGAGGGGGCCGCCCCCCCCCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
205 c 237 g 14
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Primates;
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Pred. No. 4.2e-60;
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WO0216416.
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Submitted (30-DEC-1999) Division
Second TMVS, Frome Rd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolliffe,C.N., Harvey,K.F., Haines,B.P., Parasivam,G. and Kumar,S. Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolliffe, C.N. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 351 Pt 3, 557-565 (2000) 20498735
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                                                                                                           GAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTG
                                                                                                                                                                                                                                GAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCCGAGCAGCAGCTG
                                                                                                                                                                                                                                                                                                                    TATCCGTACCTGCAGCACGAGATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAG
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                          ATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCC
                                                                                      GAGCTGAACCGGGAATCTGTGCGCGCGCCCCTAACCGGACCATCTTCGACAGTGACCTT
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(bases 1 to 651)
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/product="NedAc44247.1"
/protein_id="AAc44247.1"
/protein_id="AAc44247.1"
/db_xref="GI:12004974"
/translation="SQARREDGLISSEGCLWPSESTVSGGMPEPQVYAPPRPTDRIAV
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Location/Qualifiers
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/mol_type="mRNA"
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 107 from Patent Ax011709
                                                                                                                                                                                                                                                                                                                               Human nucleic acid sequences obtained from pancreas tumor tissue patent; WO 9955858-A 107 04-NOV-1999;
Patent; WO 9955858-A 107 04-NOV-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
LOCATION/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human osteoblast d		-			DNA encoding novel	DNA encoding novel	Human secreted exp	DNA encoding novel	Oligonucleotide fo	Oligonucleotide fo	Manic-depressive i	Human cDNA differe	DNA encoding novel	Oligonucleotide fo	Oligonucleotide fo			Human MIVR-1 homol	Manic-depressive i	Human cDNA for nov	DNA encoding novel	Human secreted pro	DNA encoding novel	Phase-1 Rat CT gen	Novel human polynu	Toxicologically re					cDNA encoding a mu	Human MIVR-1 homol				Human polynucleoti

ALIGNMENTS

RESULT 1 ABK12137 ID ABK1

ABK12137 standard; cDNA; 1321

ВP

ABK12137;

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Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac pypertrophy; myocardial infarction; stroke; arteriosclerosis;
22-AUG-2000; 2000US-227159P
                         21-AUG-2001; 2001WO-US26089.
                                                   28-FEB-2002.
                                                                         WO200216416-A2
                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                            Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
                                                                                                                                                                                                                                                                                                     05-JUN-2002 (first entry)
                                                                                                                                                                                                      failure.
                                                                                                                          Location/Qualifiers
413..1276
/*tag= a
                                                                                                  'note= "This region is specifically claimed in claim 3"
                                                                                                                 'product= "MIVR-l"
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99999999999<del>8</del>8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC they are not identical to Genbank sequences AI76144:1., AI594390, CC they are not identical to Genbank sequences AI76144:1., AI594390, CC this, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of Cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprision of such activity is comprising MIVR-1, iex-1, VDUP-1, BTG-2 and TIS-1d or its comprision of such activity is comprised to the comprision of such activity is comprised to the comprision of such activity is comprised to the comprision of such a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCGGCGGCGGCGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCAGCCCC
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AAA75151 standard; cdna; 969

AAA75151;

15-JAN-2001 (first entry)

Ď human TANGO 261 polypeptide

TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; con willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiecta congestion; bronchiectasis;

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                                                                                                                                                                                           Query Match
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Matches 805
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                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit constate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ARR92115 ARR92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

06-APR-2001;

24-APR-2001;

30-APR-2001;

30-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated gears expressed in a prostate tissue
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                                                                                                   AGGATGCCTGTGGCCCTCGGAGAGCCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGT
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                                                                                                     CGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCA
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                                                                                                      Novel human and murine secreted proteins designated TANGO 216, 266 and 267 useful as modulating agents of cellular proces
                                                                                                                                                                                           WPI; 2000-579269/54.
P-PSDB; AAB18462.
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Disclosure;

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cc dascribes Tango 266, Tango 261 proteins. The specification also collections and the collular differentiation and/or modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular and factor-associated collulate cell that ficking and/or modulate cellular differentiation. The classical cell trafficking and/or migration, modulate cellular adhesion. The condulate cell adhesion in proliferative disorders, such as cancer, cc modulate the proliferation, differentiation, modulate cellular adhesion, cc and hematopoietic associated diseases and disorders, such as cancer, cc modulate the proliferation, differentiation, and/or function of cells cashma and bronchiectasis, intestinal disorders, such as cancer, cc asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat bone marrow, blood cashma and bronchiectasis, intestinal disorders, spleen associated cc asischemic heart disease, modulate the proliferation, differentiation, cand/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorders. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disease, cerebral coreated using information provided.
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AAA75163-65 encode human TANGO 261 proteins. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells
                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 262, 266 and 267 useful as modulating agents of cellular proces e.g. for treating cancer -
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                                                                                                                                                           Disclosure; Page -; 175pp; English
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that appear in the bone marrow, and leukocytes, treat bone marrow, blood cand hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated claseases, modulate renal disorders, treat cardiovascular disorders such as ischamic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, cerebral coordens, bacterial and viral meningitis, Alzhelmer's bloease, cerebral coorders. hydrocephalus and encephalitis, and treat hepatic disorders. onte: the present sequence does not appear in the specification; it was
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11-DEC-1998;
09-FEB-1999;
16-MAR-1999;
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useful for disorders Claim 9; New human neuron-associated proteins and polynucleotides encoding the useful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders Page 136; 145pp; English.

Yang

Human neuron-associated proteins (NEUAP) can be used for for treating or preventing a disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzhelmer's disease, Plok's disease, Huntington's disease, dementia and Parkinson's disease. NEUAPs are also useful for treating other demyelinating diseases, bacterial and viral meningitis, prion

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GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGG
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                                              GCCCACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTCCCTTCCAGCACCAGCAGAG
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29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; Parkinson's gisease, corrective; nootropic; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein; gene; ss.
                                                                                                                                                                                                                                                     New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory d (e.g. AIDS), neurological disorders (e.g. AIZheimer's), or content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                             Dufour GE, Hillman
Daughtery SC, Dam'
Peralta CH, David 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple sclerosis; Parkinson's disease; Creutzfeldt-Jakob disease;
multiple sclerosis; Parkinson's disease; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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2001US-280068P.
2001US-291280P.
2001US-291839P.
2001US-291849P.
2001US-2991849P.
2001US-29976P.
2001US-390706P.
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MH, Lewis SA
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                                                                                                                                                                                                                                                                                                                                                                                                                             O, Yap PE, Amshey SR;
DA, Kleefeld Y, Gersti
AJ, Panzer SR, Harris
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The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (ABZ55837-ABZ56403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them of NAB equivalent of them. The polypeptide or polynucleotide are useful treating, preventing or diagnosing a disease or condition associated the expression of functional SFTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders

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Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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TCCCCAGGGGGCCGGGCTGGGGTGGAAAAGGCAG 1321
                                                    AGAGAGCGCAGCCATCTGGAGCAAAGAGAAGGATAAACAGAAAGGACACCCTCTTAGGG
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAAI8642-AAA42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assaus for recentral trivity artherities and inflaments.
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19-OCT-2000;
29-NOV-2000;
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                                      2000US-227159P
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Sequence 878 BP; 179

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147 T; 0 other;

encodes mouse MIVR-1.

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The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC they are not identical to Genbank sequences AI761441.1, AI594390, CC NM_00438 and AQ177461. Also included are expression vectors, host CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of CC MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining if the anti-apoptotic activity is CC modulated and thereby identifying a modulator. The cardiac cell anti-capoptotic molecules and nucleic acids of the invention are useful for CC treating, diagnosing and monitoring progression of such diseases and CC disorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, Stroke, arteriosclerosis and heart failure. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases
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ABS61424
ID ABS61
XX ABS61
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CXX Prost
XX Human
KW Cytos
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XXX Homo
OS Homo
XXX Homo
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X
The invention relates to an isolated polypeptide comprising a sequence with 60 % identity to one of prostate specific protein (PSP) sequences, corresponding an amino acid sequence encoded by one of 136 nucleotide prostate specific nucleic acids sequences, PSNA, (or a sequence that thybridises to it or is 60% identical to it), given in the specification. It comprising the vector comprising the polynucleotide, a host cell comprising the vector, an antibody specific for the PSP proteins and a vaccine comprising the protein or polynucleotide. The PSP and PSNA are useful for diagnosing and monitoring the presence and metastases of prostate cancer in a patient. The PSNA is useful for determining the presence of prostate specific protein in a sample, and cetermining the presence of prostate specific protein in a sample, and contrasting a patient with prostate cancer, which induces an immune response against the prostate cancer cell expressing the nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; prostate specific nucleic acid; PSNA; cytostatic; non-cancerous prostate disease; PSP;
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                             Human; ss; MIVR-1; Mechanically Induced Vascular Receptor 1; cytostatic; cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell; anti-apoptotic; vascular endothelial cell; cardiac hypertrophy; myocardial infarction; stroke; arterioscheart failure; AI761441.1.
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                                                                                                                           Human MIVR-1 homologous sequence
                                                                                                                                                          05-JUN-2002
                                                                                                                                                                                         ABK12143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule encoding a CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having CC cardiac cell anti-apoptotic activity and fragments of it provided CC they are not identical to Genbank sequences AI761441.1, AI594390, CC NM,004338 and AQ177461. Also included are expression vectors, host CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of CC MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its comprising mivR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its comprising mivR-1, its-11d earlier apoptotic activity is CC modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for CC apoptotic molecules and nucleic acids of the invention are useful for CC disorders as characterised by increased apoptotic cell-death of vascular CC disorders as characterised by increased apoptotic cell-death of vascular CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction, CC stroke, arteriosclerosis and heart failure. The present sequence CC is one of the four Genbank sequences (AI761441.1) which are homologous to the cDNA for human MIVR-1 and which are specifically disclaimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 533
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PFIZER INC.
TCCTCCTTCCAGCAGCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGGA-GGGGACCCGGCT
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      The present sequence encodes a murine TANGO 261 polypeptide. The specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedemma; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; halbeimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
                                                                                                                                                                                         Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
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P-PSDB; AAB18450.
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                                                                                                                                                               Fig 6A-B; 175pp; English
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Query Match

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CC describes TANGO 266, TANGO 261 proteins. The specification also CC describes TANGO 265, TANGO 267, TANGO 267. The TANGO CC polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The CC proteins can be used to treat any von Willebrand factor-associated CC disorder, regulate extracellular matrix structuring, cellular adhesion, The CC and cell trafficking and/or migration, modulate cellular interactions, cC modulate cell adhesion in proliferative disorders, such as cancer, CC modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial CC asthma and bronchiectasis, intestinal disorders, spleen associated CC asthma and bronchiectasis, intestinal disorders, spleen associated cond/or function of bone and cartilage cells and to treat bone and/or CC cartilage associated with the ovaries, and cerebral observations, brain herniations, latrogenic disease, inflammations, bacterial and viral meniagitis, Alaheimea's blease, cerebral
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                                                                                     toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page -; 175pp; English
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SUMMARIES 8 Ouery O. Score Match Length DB ID 1 866 65.6 1201 9 AL517150 2 859.4 65.1 1009 9 AL578575 3 766.8 58.0 967 13 BQ641849 4 766 58.0 1046 12 BM922276 BM922276 AGENCOURT	29: 9b_gss2:* 29: gb_gss2:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			12: 95_est3:* 13: 9b_est4:* 14: qb est5:*		1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estmu:* 5: em_estov:*	cessing: M	mum DB seq length: 0 mum DB seq length: 2000000000	l number of hits satisfying chosen parameters: 45562784	able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	.e: US-09-934-249-1 ect score: 1321 ence: 1 cgaccgcggtctcggagcgactgcgtaggtgaaaaggcag 1321	on: August 27, 2003, 17:43:55 ; Search time 3107 Seconds (without alignments) 10333.509 Million cell updates/sec	ucleic - nucleic search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
Gender Ge	REFERENCE 1 (bases 1 to 1201) AUTHORS LI,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished COMMENT On Feb 13, 2001 this sequence version replace	ACCESSION AL517150 VERSION AL517150.2 GI:30492472 VERWORDS EST SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; (RESULT 1 AL517150/c AL517150 AL517150 DEFINITION AL517150 Homo sapiens NEUROBLASTOM		41 453.4 34.3 949 13 42 452.2 34.2 618 14 43 448 33.9 626 12 44 444.2 33.6 990 13 45 467 33.5 602 14	34 473.4 35.8 1017 13 35 468.8 35.5 1280 13 36 468 35.4 857 10 37 468 35.4 974 10 37 468 35.3 744 13 38 465.8 35.3 744 13 39 461 34.9 763 123	480.8 36.4 964 1 478.6 36.2 1174 2 477.6 36.2 646 3 476.4 36.1 651	501.6 38.0 588 12 493.6 37.4 693 9 493.4 37.4 655 13	529.8 40.1 894 12 529.8 39.4 1068 13	567.4 43.0 729 13 564.8 42.8 730 12 563.2 42.6 728 13	605.8 45.9 915 13 592 44.8 888 13 578.4 43.8 890 13	11 080.0 32.0 12.0 12.0 12.0 12.0 12.0 12.0 12.0 1	715.4 54.2 1007 9 7 7 15.4 54.1 874 13 691.2 52.3 945 13 696 6 52.0 950 13	764.2 57.9 1201 9 AL54317 736.4 55.7 916 13 BQ9945 735 55.6 951 9 AL55888
scope - Centre National de Sequencage 91 91006 EVRY cedex - France 1: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr ary was constructed by Life Technologies, a division of trogen. This sequence belongs to sequence cluster 9945.r For information about this cluster, see 1.//www.genoscope.cns.fr/bbin/Cluster.cgi?seq=CS0DA008CA12NP1&cluster=9945.r. Contact: Liang Email: fliang@lifetech.com URL:	Catarrhini; Hominidae; Homo. and Polayes,D. d normalization version replaced gi:12780643.	quence. Craniata; Vertebrata; Euteleostomi;	ALIGNMENTS 1201 bp mRNA linear EST 09-MAY-2003 Sapiens NEUROBLASTOMA Homo sapiens CDNA clone		BX355486 BX356486 CD367193 UI-H-FT2- BM974296 UI-CF-EC1 BQ691066 AGENCOURT	BX400248 BQ691500 AGENCOURT BG323347 602421734 BB624904 BB624904 BU414421 603670223 BI646175 603276395	BU85986 AGENCOURT BU85986 AGENCOURT AL517151 AL517151 BU859841 AGENCOURT CB554226 MMSP0052_	BM483503 536869 MA AI761441 Wg65f07.x BQ691705 AGENCOURT BM550330 AGENCOURT	BM141979 1125811.y BI851941 603379004 BU527705 AGENCOURT	BQ575741 UI-H-E21- BQ6757602 UI-E-E01- BM677602 UI-E-E01- BU683523 UI-CF-EC1	BX36444 BX34441 BX364397 BX362397 BX362397 BX362397 BX362397 BX362397 BX362397 BX362397 BX362397 BX362397 BX362187 BX362	BUDUATE AGENCULAT AKO08976 Mus muscu BC023092 Mus muscu BQ015170 U1-H-ED1-	AL558882 AL558882 BX362396 BX362396 BU539219 AGENCOURT	AL54317 5 AGENCO AL55888

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GGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCT
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_tib="Homo sapiens NEUROBLASTOMA"
/note="Wector: pcfwSpORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i the Not I and ECONV sites of the pcMVSPORT 6 vector. Library was not normalized."

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/mol_type="mRNA"
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/clone="CSODA008YB23"
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r
more information about this cluster, see
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Genoscope - Centre National de Sequencage
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AL578575 GI:31316780
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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a 293 c 344 g 201 t 11 others
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5', mRNA sequence.
BQ641849 BQ641849.1 GI:21766021
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                                                   CCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAA
                                                                                                                 CCGTACCTGCAGCACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAG
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                                                                                               CGCCTGGCCGTGCCGCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTAT
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300 823 763 180

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120 643 60

703

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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                        /tissue_type="normal pigmented retinal epithelium"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by Oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:6292265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                              58.0%;
99.1%;
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Primates;
Score 766.8; DB 13
Pred. No. 5.5e-125;
0; Mismatches 7;
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                       Query Match
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (Dases 1 to 1046)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                       Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5', mRNA sequence.
BM922276
BM922276.1 GI:193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM922276 1046 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437
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                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 671.
Location/Qualifiers
                                                                                           /clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

05 a 391 c 298 g 150 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                     LLAM12791
                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                               /lab_host="DH10B"
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                                      58.0%;
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                       Score 766; DB 12;
Pred. No. 7.6e-125;
D; Mismatches 32;
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AL543170 Homo sapiens PLACENTA CC clone CSODIO02YIO3 5-PRIME, mRNA AL543170
AL543170. GI:31265017
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Primates;
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
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On Feb 15, 2001 the
Contact: Genoscope
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                                                                                                    TCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGG
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 415 c 332 g 182 t 50 others
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/mol_type="mrNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 916)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL http://lmage.llnl.gov plate: LLAM13626 row: c column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Location/Qualifiers
/clone_lib="Lupski_sciatic_nerve"
/note="Vector: pcMV-SPORT6 (Life Technologies); Si
NotI; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size sel
1 kb for average insert length 1.87 kb. This is a
library, non-amplified. Library constructed by Lif
                                                                                                                               /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                   /clone="IMAGE:6204609"
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Query Match Best Local Similarity

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354 c 273 g 127
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95.7%;
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CELLS (JURKAT CELL LINE) COT 10-NORN
CSODJ015YF12 3-PRIME, mRNA sequence.
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.2e-11
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is available through Life
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cgi-bin/cluster.cgi?seq-CS0DJ015DC06NP1&cluster-9945.r. Contact Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitroden Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0DJ015DC06NP1.
                                                                               GCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence clus
CCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAG
                                                                                                                                       CACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCACCTTCTCGCTTTCAGACGG
                                                                                                                                                     CACCTATCCGTACCTGCAGCACGAGATCGACCTGCCACCACCCATCTCGCTGTCAGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
On Feb 15, 2001 th:
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 951)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/mol_type-"mRNA"
/db_xref-"taxon:9606"
/db_xref-"taxon:9606"
/clone-"CSODJ015YF12"
/cell_type-"T CELLS (JURKAT CELL LINE) COT 10-NORWALIZED"
/cell_line-"JURKAT"
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10-NORMALIZED"
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99.1%;
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; Pred. No. 2.1e
1; Mismatches
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braries and normalization
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AL558882
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ORIGIN
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AL558882
AL558882.2
EST.
                                                                                                                                                                                                                                                                                   Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence clus 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODJ015DC06QP1&cluster=9945.r. Contac peng Liang Email: fliang@lifeten.com URL: http://fullength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODJ015DC06QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
On Feb 15, 2001 thi
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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AL558882 Homo sapiens T
Homo sapiens cDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1007)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCGGCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTT
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   54.2%;
nilarity 99.1%;
Conservative
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                                                                        /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the PCMYSPORT 6 vector. Library was normalized a 325 c 292 g 151 t 21 others
                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJ015YF12"
                                                                                                                                                    /clone_lib="Homo sapiens T CELLS
                                                                                                                                                                                 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
 Score 715.4; DB 9;
Pred. No. 5.8e-116;
2; Mismatches 3;
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                                                                                                                                                                Homo sapiens
BX362396
BX362396.1
EST.
Unpublished
Contact: Genoscope
Genoscope - Centre National
BP 191 91006 EVRY cedex - Fr
                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 874)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and
                                                                                                                                                                                                                           BX362396
BX362396
                                                                                                                                   Homo sapiens (human)
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             Sequencage
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/cg1-bin/cluster-9945.r. Contact cg1-bin/cluster.cg1?seq=CSODJ014CG08NP1&cluster-9945.r. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feng Liang Email : fliang@lifetech.com URL http://fulllength.invitrogen.com/ InVitroGe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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CACCTACAGCGAGGTCATCGGCCACTACCCGGGGTCCTTCCAGCAGCAGCAGCAGCAG
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Location/Qualifiers
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/cell_line="JURKAT"
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/clone="CS0DJ014YN15"
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/mol_type="mRNA"
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96.28;
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Pred. No. 6.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2757 row: p column: 18
High quality sequence stop: 663.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
               ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGA
                                                                                 GGTGATGATGGTGATGGTGGTGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGATGATGGTGGTGGTGATCACGTGCCTGAGCCACTACAAGCTGTCTGC
                                                                                                                                                                 TTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT
ACGGTCCTTCATCAGCTGGCACAGCCAGGGGGGGGGGGAGAAGATGCCCTGTCCTCAGA
                                                                                                                                  TCTCCTGCGAAACCAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT
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                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                 /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type-"mRNA"
/db_xref-"taxon:9606"
/clone-"IMAGE:6569922"
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Eutheria;
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Primates;
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AGENCOURT_10016502 NIH_MGC_142 H
IMAGE:6497853 5', mRNA sequence.
BU602918
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 850)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                    Unpublished
                                                                                                                                                                                                                                      BU602918.1
                                                                                                                        Contact: Robert Strausberg,
                                                                                                                                                                                                       Homo
                                                     CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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quality sequence stop: 499.
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/tissue_type="mixed (pool of 40 RNAS)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_142"
/clone_lib="NIH_MGC_142"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggcgctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAS (bladder-2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and 5'-AATCTAGAGCCGAGCCGAGACTGGCCATTACCGCCGGG-3' and 5'-AATCTAGAGCCGAGCCGCCCACTG-dT(30)NN-3', Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MCC_141), Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Similarity Conservative 52.0%; 96.9%; 0; Score 686.6; DB 13; Pred. No. 6.6e-111; D; Mismatches 19; Indels Length 5. Gaps

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CATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT CATCTCGCTGTCGGACGGGGGGGGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT

TCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAG TCGGGACCCCGAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAG

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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schrini, L. M., Staubil, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
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                                                                                           Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new of Genome Res. 10 (10), 1617-1630 (2000)
                                            and Hayashizaki,Y.
Functional annotat
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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         annotation of a full-length mouse (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Analysis of the mouse transcriptome based on of 60,770 full-length CDNAs
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459 c 374 g 173 t 1 others
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/db_xref="GI:12843489"
/db_xref="GI:12843489"
/db_xref="MGI:1929600"
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VRAPPNRTIFDSDLIDSTMLGGPCPPSSNSGISATCYSSGGRMEGPPPTYSEVIGHYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="stomach"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/clone="2210418I02"
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/db_xref="MGI:1902457"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bon.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert
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                            GCGCGTGCAACTGCCAGCGCTCTTTGTTCCCCAGCATGGAGATCACGGAGCTGGAGTTCG
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mmalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
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Pred. No. 5.7
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EST.
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.seq.primer: M13 FORWARD
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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/clone_lib="NCI_GAP_EDI"
/clone_Torqan: Left pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left pubic Bone; Vector: Site_1: EcoR I;
Site_2: Not I; NCI_GAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line_CS5. The library was constructed according to Bonaldo
. Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tag for this library is GCTCAAGGCT
TAG_LIB-UI-H-ED1
TAG_TISSUB-chondrosarcoma
TAG_SEO-CGTCAAGGCT*
a 223 c 271 g 176 t 3 others
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/mol_type="mRNA"
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                   751 TCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTT
                                                                                                        691 GCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCC
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Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA
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609 bp mRNA linear EST 15-JUL-2002 hdl3h06.yl Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone hdl3h06 5', mRNA sequence.
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Plate: 13 row: h column:
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                                                                                                                                                                                                                                                                                                                                     /note-"Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORR1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'.pgACTACTTCTACATCCGGCGCGCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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754 GCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCA

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Sequence 2, Application US/09769482

Patent No. 6566130

REPLICANT: SRIVASTAVA, SHIV

APPLICANT: SEGNAMA, TAKEHIKO

ITLE OF INVENTION: POYNUCLEOTIDE ARRAY

FILE OF INVENTION POYNUCLEOTIDE ARRAY

FILE REFERENCE: 04995.0057-00000

CURRENT APPLICATION NUMBER: US/09/769,482

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,772

PRIOR APPLICATION NUMBER: 60/179,045

PRIOR APPLICATION NUMBER: 60/179,045

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2

LENGTH: 759

TYPE: DNA

"ORGANISM: Homo Sapiens
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                                                    Conservative
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99.7%;
                                                Score 755.8; DB 4;
Pred. No. 2.6e-133;
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US-09-091-952A-7
; Sequence 7, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
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                                                                       NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
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                                                                                                            TITLE
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ADDRESSEE: Townsend and Townsend and STREET: Two Embarcadero Center, Eight CITY: San Francisco STATE: CA COUNTRY: USA ZIP: 94111-3834
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                                                                                                       Berrettini, Wade H.
YOShiKawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
INVENTION: Chromosomal Markers and Diagnostic
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                                                                                                                                                                    Badner, Judith
Goldin, Lynn R
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                                                                                   Tests for Manic-Depressive Illness: 197
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; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-091-952A-7
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Matches 482; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-CCT-1996
APPLICATION UNMBER: PCT/US97/19381
FILING DATE: 28-CCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
WATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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986 TTCGACAGTGACCTGATGGATAGTGCCAGG---CTGGGCGGCCCCTGCCCCCCAGCAGT 1042
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                                                                                                                                                                                                                                     GCCCCGCGGTCCAGGGACAGGTTCACAGCGCCCGTCCTTCATCCAGAGGGATCGCTTCAGC
                                                                                                                                                                                                                                                                                                                   CCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCGCTTCCAC
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                    CCCGAGCAGCAGCTGGAACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATC
                                                                                                                CTGTCCGACGGTGAAGAGCCACCTCCTTACCAGGGGCCCCTGCACCCTGCAGCTCCGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, Timothy L. REGISTRATION NUMBER: 35,367
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 4
US-09-091-952A-6
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                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
FEATURE:
                                                                          FEATURE
                                                                                                                                                       MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, Timothy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/091,952A FILING DATE: 19-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAGCGCAG
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                OTHER INFORMATION:
                                    NAME/KEY:
                                                                                               OTHER INFORMATION:
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/029,278 FILING DATE: 28-OCT-1996
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                                                                                                                 LOCATION:
                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US97/19381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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Yoshikawa, Takeo
Yoshikawa, Alan R.
Sanders, Alan R.
Esterling, Lisa E.
Esterling, Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
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COCATION: 5595...5685
COCHER INFORMATION: ampl.
SEQUENCE DESCRIPTION: SEQ ID 1950...5685
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      Sanders, Alan R.
Esterling, Lisa E.
INVENTION: Chromosomal
                                                                     Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
                                                                                                                                                         Detera-Wadleigh, Se
Gershon, Elliot S
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Pred. No. 1.3e-57;
0; Mismatches 168
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APPLICATION NUMBER: US/09/091,952A

FILING DATE: 19-Apr-1999

CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

FILING DATE: 28-0CT-1996

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-0CT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
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CGCTTCCAGCCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCC
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OTHER INFORMATION: C. spliced coding region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows
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LENGTH: 4403765
TYPE: DNA
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
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OTHER INFORMATION: "n" bases at various positions
OTHER INFORMATION: represent a, t, c or g
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                                                  CTGAGCCCCGCGGCGCCCCGGGAACTTGGCGGCGACCCGAGCCCGGCGAGCCGGGGGCGCG
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LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA SEQUENCES TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                  GCCTCCTCAGCTACCAACGGCGGCAGCGGCGGCGCGG--CGGCACCGGAGGCGACGGCG
                                                                                                                                                                                             CTGAGCCCCGCGCGCCCCCGGGAACTTGGCCGCGGCCGAGCCCGAGCCGGGGGCCGCG
GCGGACAAGGTGGCCAGGGCGCGCGGCGGCGGTGCCGG
                                                                                       GGCGGCGCCGGCAGCGGGCCCAACACCAGTCCCGGCGGCAACGGCGGCCAAGGAGGT
                                                                                                                                                                                                                                                                                                                        GCGGCAGCGCGCCCCCCTGCCAGCCCATTTTCCGGACGCCACCCCGCGGCACTGCCG-
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                                                            GCGGACAAGGTGGCCAGGGCGCGGCGGCGGCGGTGCCGG
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49.8%;
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Pred. No. 0.00033;
0; Mismatches 227;
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Best Local Similarity 49.2
Matches 234; Conservative
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                            LOCATION: FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCI(DOS) TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                              19499 CTCGGGTGCGGAACGTCCCGCGAGCCGCGGCGAGCGTCCCGGCGGCGTCGGCCGGGGC 19440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
185 CCCCGGGGCTGCCGAGGGGAGGCCGGGGGGGGGGCGCAGCGGAGCGCGGTCCCGCGCACTGAG
                                                                                                                   65 GGCGGCGGCGGAGGCGCTCGGCTGGGGAAAGCTAGCGGCAGAGGCTCAGCCCCGGCG
                                                                                                                                                                            5 CGCGGTCTCGGAGCGAAACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGAGGAGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                        GCAGCGCGCCCCCCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCACTGCCGACGC 184
                            GCGGGCGTCCGCCGGTACGCCGGCCAGGTCACGCAGGACCTCCGGGAGAGCGGTGGCACC 19320
                                                                                       : 44377 base pairs
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36155..41830
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20110..31284
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                                                                                                                                                                                                                               Score 68; DB 2;
Pred. No. 0.00025;
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                                                                                                                                                                                                                Mismatches 240;
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RESULT 9
US-08-804-198-1/c
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GENERAL II
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                          FEATURE:
                                                        FEATURE:
                                                                                       LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: CANTRELL, PAUL R.
                                                                                                                       EATURE:
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
             NAME/KEY:
                                  LOCATION:
                                               NAME/KEY:
                                                                LOCATION:
                                                                              NAME/KEY:
                                                                                                            NAME/KEY:
                                                                                                                                          TOPOLOGY:
                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                         COMPUTER: Macintosh 7.0 OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1
                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                            ENGTH: 44377 base pairs
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LILLY CORPORATE CENTER
                                                                                               CDS
350..14002
CDS
31329..36071
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14046..20036
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317-00: 1:
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/ENTION: PLATENOLIDE SYNTHASE GENE
                                20110..31284
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                                                                                                                                                                                                                                                                                                                                            Floppy disk
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US-08-690-473-1/c
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NAME/KEY:
LOCATION:
                          ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,64:
                                                                                                       SOFTWARE: PatentIn Relicuration DATA:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                      COUNTRY: US
                                                               APPLICATION NUMBER: FILING DATE: 26-JU CLASSIFICATION: 43
                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                 Houston
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                                                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                               P.O. Box 4433
                                                                                                                                                                                                                                                                                                                           Leopardi,
Roizman, B
                                                                                                                                                                                                      USA
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36155..41830
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                                                                             26-JUL-1996
  INFORMATION
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                                                                                                                                                                                                                                                                                                                              Bernard
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                                                                                             us/08/690,473
                         37,642
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            ARCD: 239
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Pred. No.
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                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES S
FILE REFERENCE: ARCD:317
                                                                                      SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                Sequence 1, Application US/09259821A Patent No. 6210926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/259,821A CURRENT FILING DATE: 1999-03-01
                                                                                                                               PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-
                                                                                                                   NUMBER OF SEQ ID NOS:
                                         TYPE: DNA
ORGANISM: HERPES
                                                                        LENGTH:
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                                                                                                                                                                                                                                     LEOPARDI, ROSARIO
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ARCD: 317
                                            VIRUS,
                                                                                                                                 1996-07-26
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                                            TYPE
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Pred. No. 0.00022;
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67.6;
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SEQUENCE CHARACTERISTICS:

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RESULT 12
US-08-843-659-1/c
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          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
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                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                               APPLICANT: Roizman, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
 TELEFAX:
                                                                                                     FILING DATE:
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        COUNTRY:
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(512) 474-7577
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INHIBITORS OF APOPTOSIS
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US-08-458-568A-11
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                                                                                                                                                                                                                                                                                                          Sequence 11, Applicat Patent No. 5821339
GENERAL INFORMATION:
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Best Local Similarity
Matches 239; Conserv
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ICOMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDER-FECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn,
                                                                                                                                                                                                                                               TITLE OF INVENTION: Composition TITLE OF INVENTION: Infections
                                                                                                                                                                                                                                                                             APPLICANT: Schaffer, APPLICANT: Yeh, Lily
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                 STREET: One _____
                                                                                                                COUNTRY: UZIP: 19103
   APPLICATION
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                                                                                                                                                                              One Liberty Place, 46th
                                                                                                                                 USA
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   NUMBER:
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US/08/458,568A

    Mismatches

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                                                                                                                                                                                               Kurtz,
                                                                                                                                                                                                                                                              Methods
                                                                                                                                                                                               Mackiewicz
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RESULT 14
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294338
; GENERAL INFORMATION:
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ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Leary Ph.D., Kathryn I REGISTRATION NUMBER: 36,317 REFERENCE/DOCKET NUMBER: DFO TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
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Pred. No. 0.00025;
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APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN

FILE REFERENCE: 24365-20007.00

CURRENT APPLICATION UNMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 1

LENGTH!
                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-128-155-16
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                      Sequence 16, Application Patent No. 6117654
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Best Local
                                                     CURRENT APPLICATION NUMBER: US/09/128,155 CURRENT FILING DATE: 1998-08 3 EARLIER APPLICATION NUMBER: US 60/091,650 EARLIER FILING DATE: 1998-07-02 EARLIER APPLICATION NUMBER: US 60/054,646 EARLIER FILING DATE: 1997-08-04
                                                                                                                                                                  TITLE OF INVENTION: NOVEL MOLECULES TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
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Pred. No.
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; FEATURE:
NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
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Search completed: August 27, 2003, 20:11:11 Job time : 133 secs
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Best Local Similarity 49.1%;
Matches 189; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                            22183 CCCCCCGGGCCCCCCCCGCGG 22207
                                                                           135 CCCCGCTGCCAGCCCATTTTCCGGACGCCACCCGCGGGCACTGCCGACGCCCCCGGGGCT 194
                                                                                         435 ACAGCACCGCCGCCGCCGCCGG 459
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Pred. No. 0.0007;
0; Mismatches 191; Indels 5
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Match
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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'cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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US-09-796-753-55
US-10-301-822-208
US-10-205-823-412
US-10-205-824-1-71
US-10-241-220-45
US-09-934-249-14
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		5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.2	5.2	υ. Έ	5.3	5 .5	5.5	5.5	5.5	5.7	5.7	5.7	5.9	13.8
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US-10-023-529-45	US-09-976-740-45		US-10-032-393-8	US-10-032-393-47	US-10-225-567A-43	US-10-156-761-3259	US-09-880-107-3950	US-09-954-456-529	US-09-954-456-292	US-10-017-161-1857	US-09-825-288A-1	US-10-017-161-1483	US-10-156-761-3424	US-09-954-531-1351	US-10-171-311-15	US-10-097-340-11	US-10-017-161-1403	US-10-156-761-1	US-10-156-761-4388	US-10-023-523-48	US-10-023-529-48	US-09-976-740-48	US-09-893-519A-87	US-10-023-523-48	US-10-023-529-48	US-09-976-740-48	US-09-796-679-5	US-09-918-995-2074
Sequence 45, Appl	4	Sequence 1, Appli	Sequence 8, Appli	47	Sequence 43, Appl	3259,	3950,			18		14	34	Sequence 1351, Ap	15,	11,	ô	Sequence 1, Appli	438		48,	Sequence 48, Appl	87,		48,	Sequence 48, Appl	Sequence 5, Appli	Sequence 2074, Ap

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE: COS
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US-09-934-249-1
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APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine
APPLICANT: Turi, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application us
Patent No. US20020115081A1
                                                                                                                                                  Query Match 100
Best Local Similarity 100
Matches 1321; Conservative
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APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
1 CGACCGCGGTCTCGGAGCGAAACCCGGATCTCCTTTGGACTTGAATGAGGAGGAGGAGGAGGCGG
                                                                          1 CGACCGCGGTCTCGGAGCGAAACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGGCGG
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                                                                                                                                                                    100.0%; Score 1321; DB 10; 100.0%; Pred. No., 9.2e-282;
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CTTCCAGCACCAGCAGAGCAGTGGGGCCCCCCCTCCTTGCTGGAGGGGACCCGGCTCCACCA
                                                                        CGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGG
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APPLICANT: Williams, P.Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo 9
US-10-241-220-119
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P.Mickey
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Best Local Similarity
Matches 1229; Conserv
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 TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATGATGGTGA
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Sequence 3, Application US/0934249
Patent NO. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 86
TYPE: DNA
ORGANISM:
FEATURE:
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NUMBER OF SEQ ID
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LENGTH: 969
TYPE: DNA
ORGANISM: Homo
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PRIOR APPLICATION NUMBER: 09/:
PRIOR APPLICATION NUMBER: 1998-12-30
NAME/KEY: CDS
LOCATION: (6)...(761)
-09-796-753-55
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
                                                                                                                                 PRIOR FILING DATE:
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PRIOR FILING DATE: 1999-03-01
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PRIOR APPLICATION NUMBER:
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FILING DATE: 2000-07
APPLICATION
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APPLICATION NUMBER: 09/
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APPLICATION NUMBER: 09/474,071
FILING DATE: 1999-12-29
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VENTION: SECRETED PROTEINS

NCE: 7853-227-999
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Sequence 208, A Publication No.

Application US/10301822 5. US20030148410A1

Inc.

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.

APPLICANT

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LOCATION: (96)...(854)
US-10-301-822-208
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CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-20
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Best Local Similarity
Matches 810; Conserv
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SEQ ID NO 208
LENGTH: 1141
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TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMI
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MPM01-029P2RNM
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CAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGGGGGCGCATGGAGGGGCCGCC
                                                                                          CAGTAACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGCGGCGGCGCATGGAGGGGCCCCC
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SEQ ID NO 412
SEQ ID NO 412
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-205-823-412
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PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
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                                                                                                                                                                                                                                                                                                Query Match
Best Local
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TITLE OF INVENTION: MCPL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMI
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
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PRIOR FILING DATE: 200
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Endege, Wilson O.
Gannavarapu, Manjula
Gorbatcheva, Bella
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                              AGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCCAGAGCCGCAGGT
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Kamatkar, Shubhangi
Wonsey, Angela M.
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Pred. No. 1.4
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Mismatches 12
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-44
                                                            Query Match
Best Local S
Matches 810
                                                                                                                                                                                                                                                                                                RESULT 7
US-10-241-220-44
                                                                                                                                                                                               APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heldi
PPLICANT: Polakis, Paul
PPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
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                                                                                                                                                                                                                                                                    Sequence 44, Application US/10241220 Publication No. US20030148408A1 GENERAL INFORMATION:
                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILLE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
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              499 TTTGTTCCAGAGCATGGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATGGT 558
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                                                                    Similarity
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98.4%;
                                                     Score 802.2; DB 12;
Pred. No. 1.4e-167;
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                                         Sequence 71, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Xu, Chongjun
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhao, Oing A.
APPLICANT: Zhao, Oing A.
APPLICANT: Chen, Felyan
APPLICANT: Chen, Rui-hong
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Zhou, Ping
Ma, Yunqing
Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
Wang, Dunrui
Wang, Zhiwei
Wehrman, Tom
Zhang, Jie
Qian, Xiaohong
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CURRENT APPLICATION NUMBER: US/10/098,84
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 71
LENGTH: 1066
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TITLE OF INVENTION: NO. US20020197679A1el Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (154)..(867)
10-098-841-71
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                                            GCCACTACCCGGGGTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCGCCCTCCTTGCTGG
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                                                                                                                           CGTGCTACGGCAGCGGCGCGCATGGAGGGGCCGCCGCCCACCTACAGCGAGGTCATCG
                                                                                                                                                                                          TGGATAGTGCCAGGCTGGGCGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA
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                                                                                                                                                                                                                                                                                                                     AGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCTTCGGGACCCCGAGCAGCAGCAGCTGG
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TGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA
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Pred. No. 5.
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5.5e-165;
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; ORGANISM: Homo
US-10-241-220-45
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS.
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 45
LENGTH: 806
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 777; Conserv
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APPLICANT:
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Spencer, Susan
Williams, P. Mickey
                     ACGGTCCTTCATCAGCCGGCACAGCCAGGGGGGGGGGAGAGAAGATGCCCTGTCCTCAGA
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                                                                       CTACGCCCCGCCTCGGCCCACCGACCGCCTGCCCGTGCCGCCCTTCCGCCCAGCGGGAGCG
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                                                                                              CATCTCGCTGTCAGACGGGGAGGAGCCCCCACCCTACCAGGGCCCCTGCACCCTCCAGCT
                                                                                                                                                                       CTACGCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGCCCTTCGCCCAGCGGGAGCG
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AACCATCTTCGACAGTGACCTGATGGATAGTGCCAGGCTGGGCGGCCCCTGCCCCCCAG
                                                                                                                      CTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAGCACGAGATCGACCTGCCGCCCAC
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98.0%;
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Pred. No. 6.4e
0; Mismatches
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6.4e-160;
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Best Local Similarity
Matches 740; Conserv
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LOCATION: (20)...(841)
09-934-249-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09934249 Patent No. US20020115081A1
                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lee, Richard T.
                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                               GTTCAGATCATCATCATCGTGGTGGTGATGATGGTGATGGTGGTGATCACGTGCCTG
AGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGC
                                     TGCGCGTGCAACTGCCAGCGCTCTTGTTCCCCAGCATGGAGATCACGGAGCTGGAGTTC
                                                                                                                         TGCACGTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTT 535
                      CTGAGCCACTACAAGCTGTCAGCCCGCTCCTTCATCAGCCGACACAGCCAGGCCAGGAGG
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Turi, Thomas G.
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                                                                                                                                                                                                     Score 616.4; DB 10;
Pred. No. 1.1e-126;
0; Mismatches 111;
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                                                                                                                                                                                                                         Length 878;
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-000-256A-32
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Re-
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
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US-10-000-256A-32
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                                               Query Match
Best Local Similarity
Matches 591; Conserv
                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 32 LENGTH: 1583
                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/10000256A Publication No. US20030039983A1 GENERAL INFORMATION:
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728 GAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCGACCGCCTGGCCGTGCCGTCCGCCTTCGCC
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                                                Conservative
                                                          44.68;
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                                                            Score 589.2; DB 14; Pred. No. 1.1e-120;
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                             Query Match
Best Local Sin
Matches 533;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14
                                                                                                                                                                                                                               APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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                                                                                 NAME/KEY: unsure LOCATION: (639)...(6 OTHER INFORMATION: 6-09-934-249-14
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                                                                                                                                                                        LENGTH: 693
TYPE: DNA
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PRIOR APPLICATION NUMBER: 09/2
PRIOR STITUS DATE: 1998-12-30
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CURRENT FILLING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
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APPLICATION NUMBER: 09/3
FILING DATE: 1998-12-30
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FILING DATE: 1999-06-18
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FILING DATE: 1998-12-30
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VENTION: SECRETED PROTEINS AND USES
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NUMBER:
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US-09-796-753-57
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Matches 573; Conserv
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LENGTH: 1713
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R FILING DATE: 2000-03-01

DR APPLICATION NUMBER: 09/51

DR FILING DATE: 2000-05-14

DR APPLICATION NUMBER: 09/59

DR FILING DATE: 2000-06-19
1015 GCTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGGGGCACGTGCTACGGCAG
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APPLICATION NUMBER: 09/22
APPLICATION NUMBER: 09/630,334
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    Mismatches

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Pred. No. 1.3e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                   83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                   27;
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                                                                                                                                                                                                                                           Matches 474;
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                           LENGTH: 8093
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (6477)...(647)
OTHER INFORMATION: c or
                                                                                                                                                                                                                                                          Local
          762
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Similarity 73.7%;
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c or t/u
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Pred. No. 7.9e-68;
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1255 ACAGAAA 634 ACAGAAA	589 CCATCAC	1195 CCACCAC	529 Crccrcc	1135 GTCCTCC	469 CGGTGGC	1075 CGGCGG	409 GCTGGG
1255 ACAGAAAGGACACCCTCTAGG 1277 	589 CCATCACTCGCACATTGCCCCCACTGGAGAACAAGGAGAAGGAGAAGGAGAA 633	GAGCGCAGCCATCTG	529 CTCCTTCCAGCACCAGCAAAGTAACGGGCCATCCTGCTAGAGGGGACCCGGCT	1135 GTCCTCCTTCCAGCACCAGCAGAGCAGTGGGCCCTCCCTTGCTGGAGGGGACCCGGCT 1194	469 CGGTGGGCGCATGGAGGGCCGCCCCACCTACAGCGAGGTCATTGGCCACTACCCTGG 528	1075 CGGCGGCGCATGGAGGGCCGCCCCCCCCTACAGCGAGGTCATCGGCCACTACCCGGG	409 GCTGGGGGGCCCCTGTCCCCCCAGCAGTAACTCGGGCATCAGCGCCACCTGCTACAGCAG 468
	633	1254	588	1194	528	1134	468

APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21 NUMBER OF SEQ ID NOS: 17 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 16 Sequence 16, Application US/09934249 Patent No. US20020115081A1 PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEC. 7

310 TCATCGTCTGCCTGCAACCACTACAAAGTCTCCACGGGTCCTTCATCAACCGCCCGA 582 TGATCACGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCCTTCATCAGCCGGCACA 641 250 CGGAGCTGGAGTTCGCCCAAATCATCATCGTCGTGGTGGTGACGGTGATGGTGGTGG 522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGATGATGATGGTGATGGTGGTGG GCCAGGGGCGGAGGAGAAGAAGATGCCCTCTCAGAAGGATGCCTGTGGCCCTCGGAGA 701 ACCGCCTGGCCGTGCCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCT GCGCCGCACCGCGGCTGGG------CGCCTCGGAGATCATGCATGCCCCGCGGTCCAGGG ACCAGAGCCGGAGGCGGGACGACGGCTGCCGCAGGAAGGGTGCCTGTGGCCTTCAGACA 429 GCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTACGCCCCGCCTCGGCCCACCG 761 Mismatches Indels 9; Gaps 821 483 369 309

Length 8093;

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APPLICANT: Landschulz, Katherine T.
APPLICANT: Turi, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS FILE REFERENCE: P0738/7001_ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
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US-09-934-249-15
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PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 475
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09934249 Patent No. US20020115081A1
                                                                                                                                                                                                                                                                         Matches 408;
                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus Musculus -09-934-249-15
                                                                                                                                                                                                                                                                                      Match 25.9%;
Local Similarity 85.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGATAGTGCCAGG---CTGGGCGGCCCCTGCCCCCCAGCAGTAACTCGGGCATCAGCG 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTGAACCGGGAGTCGGTGCGCGCACCCCCAAACAGAACCATCTTCGACAGTGACCTGA 1001
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AGAGAAGATGCCCTGTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGCACCTGCAGCAGTAACGGGAGGATGGAGGGCCCACCCCCCACATACAGCGAGGTGA 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCGTACCTGCAGCACGAGATCGACCTGCCACCCATCTCGCTGTCAGACGGGGAGG 881
                                                                                                                    GTTCAGATCATCATCGTGGTGGTGATGATGGTGGTGGTGGTGATCACGTGCCTG
                                                                                                                                                  TGCGCGTGCAACTGCCAGCGCTCTTTGTTCCCCCAGCATGGAGATCACGGAGCTGGAGTTC
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                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                      Score 341.8; DB Pred. No. 3e-66;
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                                                                                                                                                                                                                                                                         57; Indels 12;
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CACGAGATCGACCTGCCACCCACCATCTCGCTGTCAGACGGGGAGGAGCCCCCACCC 892
                                                      CCGCCCTTCGCCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACCTATCCGTACCTGCAG
                                                                                                 AGAGACGATGGACTGTCCTCGGAAGGATGCCTCTGGCCCTCAGAGAGTACGGTGTCAGG-
                                          --TGGAATGCCGGAGCCACAGGTCTATGCCCCGCCTCGGCCCACTGACCGACTCGCTGTG
                                                               835
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                                          418
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arch completed: August 27, 2003, 21:35:09 time: 390 secs

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